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Db 675 AlaSerLeuValProAsnSerLeuTyrGlySerIleLeuAspIleArgSerAlaHisSer 694
QY 1979 CTTATGGAGACTGCAACAGAGGTTGACGAGACCGTGTCTTTTGGTGTGCTGGATTA 2038
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QY 2039 TCTACTTCTTCCATAAGGATAGTACAAAAACAGCGCGGTTTCGCCATTTGAGTGGC 2098
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QY 2330 AACCTTAGCTACACCCATACGGAATAACGATCTGAAACCAAGTATACAAATATCTCTACT 2389
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Job time : 99 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 16, 2003, 10:31:24 ; Search time 89.5 seconds

(without alignments)

12468.178 Million cell updates/sec

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Perfect score: 5409

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 1368560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications AA -QFAST=fastan -SUFFIX=rapb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:

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3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	4774	88.3	928	12	US-09-428-122-2	Sequence 2, Appli
2	1965	36.3	936	9	US-09-452-380-3	Sequence 3, Appli
3	1965	36.3	936	12	US-10-324-129-3	Sequence 3, Appli
4	1946.5	36.0	925	9	US-09-452-380-4	Sequence 4, Appli
5	1946.5	36.0	925	12	US-10-324-129-4	Sequence 4, Appli
6	1915	35.4	926	12	US-09-738-269-57	Sequence 57, Appl
7	1915	35.4	926	14	US-10-023-437-57	Sequence 57, Appl
8	1659.5	30.7	839	12	US-09-738-269-23	Sequence 23, Appl
9	1659.5	30.7	839	14	US-10-023-437-23	Sequence 23, Appl
10	1437.5	26.6	922	9	US-09-886-468-19	Sequence 19, Appl
11	1126.5	20.8	1006	9	US-09-841-132-190	Sequence 190, App
12	1124.5	20.8	982	9	US-09-841-132-176	Sequence 176, App
13	865	16.0	880	9	US-09-841-132-189	Sequence 189, App
14	856	15.8	866	9	US-09-841-132-189	Sequence 189, App
15	851.5	15.7	679	12	US-09-738-269-53	Sequence 53, Appl
16	851.5	15.7	679	14	US-10-023-437-53	Sequence 53, Appl
17	727.5	13.4	439	9	US-09-841-132-524	Sequence 524, App
18	685.5	12.7	931	10	US-09-779-081-2	Sequence 2, Appli
19	685.5	12.7	1609	12	US-09-841-260-75	Sequence 75, Appl
20	685.5	12.7	1609	14	US-10-007-693-75	Sequence 75, Appl
21	672.5	12.4	978	12	US-09-841-260-65	Sequence 65, Appl
22	672.5	12.4	978	14	US-10-007-693-65	Sequence 65, Appl
23	666	12.3	1723	9	US-09-841-132-395	Sequence 395, App
24	666	12.3	1723	9	US-09-841-132-395	Sequence 395, App
25	608	11.2	871	9	US-09-886-468-21	Sequence 21, Appl
26	597	11.0	1016	12	US-09-841-260-95	Sequence 95, Appl
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28	582	10.8	1530	9	US-09-841-132-178	Sequence 178, App
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30	576.5	10.7	1531	12	US-09-841-260-98	Sequence 98, Appl
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33	559	10.3	1751	9	US-09-841-132-445	Sequence 445, App
34	559	10.3	1752	9	US-09-841-132-180	Sequence 180, App
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36	546.5	10.1	977	9	US-09-841-132-191	Sequence 191, App
37	523	9.7	1770	9	US-09-841-132-444	Sequence 444, App
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39	502	9.3	848	9	US-09-841-132-192	Sequence 192, App
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41	477.5	8.8	514	9	US-09-886-468-23	Sequence 23, Appl
42	394	7.3	691	9	US-09-841-132-313	Sequence 313, App
43	385	7.1	162	12	US-09-738-269-55	Sequence 55, Appl
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45	344	6.4	700	9	US-09-841-132-345	Sequence 345, App

ALIGNMENTS

RESULT 1

US-09-428-122-2

; Sequence 2, Application US/09428122

; Publication No. US20030170259A1

; GENERAL INFORMATION:

; APPLICANT: Connaught Laboratories Limited

; APPLICANT: Mordin et al.

; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND

; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND

; FILE REFERENCE: 19721-007-019

; CURRENT APPLICATION NUMBER: US/09/428,122

; CURRENT FILING DATE: 1999-10-27

; EARLIER APPLICATION NUMBER: 60/106,046

; EARLIER FILING DATE: 1998-10-28

; EARLIER APPLICATION NUMBER: 60/132,721

; EARLIER FILING DATE: 1999-05-03

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 928

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; US-09-428-122-2

Alignment Scores:

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 Score: 4774.00 Matches: 928
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.26% Indels: 0
 DB: 12 Gaps: 0

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RESULT 2

US-09-452-380-3
; Sequence 3, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: COMEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; USES THEREOF
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

LENGTH: 936
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-452-380-3
Alignment Scores:
Pred. No.: 6.38e-153 Length: 936
Score: 1965.00 Matches: 411
Percent Similarity: 62.30% Conservative: 179
Best Local Similarity: 43.40% Mismatches: 327
Query Match: 36.33% Indels: 30
DB: 9 Gaps: 16
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QY 158 ATGATGTCTACGACAGACAGTTTTCGATTCAAGT---GCGAGTTTCGATGGGAATATAAAT 214
Db 21 ILEVALALALAGLUVALTHRLEUASPSESRASNASNSERTYRASPGLYSERASNGLY 40
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QY 272 GGAATGTCACTCTAGAAATATTTCCTGGAACAGGCACAGCAATCACAAAAGCTGTTTT 331
Db 61 SerAspValSerPheGlnAsnAlaGlyAlaLeuGlyIleProLeuAlaSerGlyCysPhe 80
QY 332 AACACACTAAGGCGATTTCACCTTTCACAGTTACGGAACCTCTATTGTTCCAAAGC 391
Db 81 LeuGluAlaGlyIleAspLeuThrPheGlnGlyAsnGlnHisAlaLeuLysPheAlaPhe 100
QY 392 GTGATGTGAGGCACTGTAGCAGCGGCTCTGCTTAACAGCAGCGGTGTAGATAAATCTACC 451
Db 101 ILEASNALAGLYSERSERALAGLYTHRVALASERTHRSERALALASPLYASNLEU 120
QY 452 AGTTTATAGGTTTTCCTGCTATCTTTTATGCGTCTCTGGAAGTTCGATAACT--- 508
Db 121 LeuPheAsnAspPheSerArgLeuSerIleIleSerCysProSerLeuLeuSerPro 140
QY 509 ACCGCAAGGAGCGGTAGTCTACGGGTAGCTTGTGTTTACAAAAGGAGTCACT 568
Db 141 ThrGlyGlnCysAlaLeuLys---SerValGlyAsnLeuSerLeuThrGlyAsnSerGln 159
QY 569 TTGCTCTTCAGCAAAACTTTTCAACGGAATAATGCGGTGCTATCCGCAAAAACCTCT 628
Db 160 ILEILEPHETHRGLNASNPHESERASPNASNGLYGLYVALILEASNTHRLYASNPH 179
QY 629 TCATTTAACAGGACTACAAATGTACGCTCTGTTTCTGAAATACG-----TCCTCAAG 682
Db 180 LeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThrGlyLys 199
QY 683 AAAGCGGAGCGCATTCACACTTCGATCCCTTACCATTTACTGGAACCAAGGGGAGTC 742
Db 200 GlnGlyValValTyAlaThrGlyThrIleThrIleGluAsnSerProGlyIleVal 219
QY 743 TCTTTTTCGACAATCTCTTCCTCGGATTCCTGAGCTGCAATTTTACAGAGCCCTCGGTG 802
Db 220 SerPheSerGlnAsnLeuAlaLysGlySerGlyAlaLeuTySerThrAspAsnCys 239
QY 803 ACTATTTCTAATAGCTTAAAGTTTCTTTTATGACATATAGGTACAGGAGCGGCTCC 862
Db 240 SerIleThrAspAsnPheGlnValIlePheAspGlyAsnSerAlaTrpGluAlaGln 259
QY 863 TCAACAACGGGGATATGTACAGGAGGTCTATCTGTGCTTATATAAACTAGTACAGACT 922
Db 260 Ala-----GlnGlyGlyAlaIleCysCys-----ThrThrThrAspLys 272
QY 923 AAGGTACCTCCTCGGAAATTCAGATGTTACTTTCAGCAACAATATACATCCAGCAACGC 982

Db 273 ThrValThrLeuThrGlyAsnLysLeuSerPheThrAsnAsnThrAlaLeuThrTyr 292
QY 983 GGAGAGCTACTATGTGAAAAGCTGAACTGGCTCCGGAGGACTTACCTATTTCAGT 1042
Db 293 GlyGlyAlaIleSerGlyLeuLysValSerIleSerAlaGlyGlyProThrLeuPheGln 312
QY 1043 AGAAATAGTGTCAATGGAGGTACAGCTCTCTAAA-----GGTGGAGCATAGCTATCGAA 1096
Db 313 SerAsn--IleSerGlySerSerAlaGlyGlnGlyGlyGlyAlaIleAsnIleAla 331
QY 1097 GATAGTGGGAAATGAGTTATCCGCCATAGTGGTGCATTCCTTTTGGGAAATACA 1156
Db 332 SerAlaGlyGluLeuAlaLeuSerAlaThrSerGlyAspIleThrPheAsnAsnGln 351
QY 1157 GTCACCTCTACTACTCTGGGAGCAAGATAGAAAGTGTATCGATTCAGCAACGAGTGCAGAG 1216
Db 352 ValThrAsnGlySerThrSerThr---ArgAsnAlaIleAsnIleAspThrAlaLys 370
QY 1217 ATGACAGCTTTCGCTGCTGCTGCTAGAGCCATCTACTTCTATGATCCCATTAATACA 1276
Db 371 ValThrSerIleArgAlaAlaThrGlyGlnSerIleTyrPheTyrAspProIleThrAsn 390
QY 1277 GCATCATCACACAGGTACAGATCTCTTAAAGTTAATGAGACTCCGGCAGATTCGCA 1336
Db 391 ProGlyThrAlaAlaSerThrAspThrLeuAsnLeuAsnLeuAlaAspAlaAsnSerGlu 410
QY 1337 CTACAAATACAGGAACATCATCTTCACAGGAGAAAAGTTATCAGACAGAGCGCGCA 1396
Db 411 IleGlyTyrGlyGlyAlaIleValPheSerGlyGlyLysLeuSerProThrGlyLysAla 430
QY 1397 GATTCCTAAATCTTACTTCGAGCTACTACAGCTGTAACTCTTTCAGGAGGTACTCTA 1456
Db 431 IleAlaAlaAsnValThrSerThrIleArgGlnProAlaValLeuAlaArgGlyAspLeu 450
QY 1457 TCTTTAAACATGAGTACTCTGACAGCTCAGGCAATTCATCTCAACAGCGCAGATTCGT 1516
Db 451 ValLeuArgAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg 470
QY 1517 CTCGAAATGGAGCTAGGAACTCTCTAGAACCTGCTGTATATAGC---ACATAAACAAT 1573
Db 471 IleLeuMetAspGlyGlyThrThrLeuSerAlaLysGluAlaAsnLeuSerLeuAsnGly 490
QY 1574 TTGGTCAATTAACATCAGTTCTATAGACGTGCAAGAGGCAAAAATAAGAAACCAAGCT 1633
Db 491 LeuAlaValAsnLeuSerSerLeuAspGlyThrAsnLysAlaAlaLeuLysThrGluAla 510
QY 1634 ACCTCAAAAATCTGACTTTATCGAACCATCATCTTTATGGACCCGACGGCAGCTTT 1693
Db 511 AlaAspLysAsnIleSerLeuSerGlyThrIleAlaLeuIleAspThrGluGlySerPhe 530
QY 1694 TATGAATCATAGTTTAAGAAATCCTCAGTCTCAGACATCTTAGAGCTCAAA----- 1747
Db 531 TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrAla 550
QY 1748 ---GCTTCTGGAAGTAAACAGCCAGCGAGTACTCCAGATCCCTATAATGGGTGAGAA 1804
Db 551 GlyAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrLeuGlnProGlu 570
QY 1805 TTCCATTAGCTATCAGGAACTTGGGGCCCAATGTTTGGGGACAGGGGCTTCTACG 1864
Db 571 ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
QY 1865 ---ACTGCAACTTCAACTGGACTAAACTGGCTATATCTTAATCCCGAGCGTATCGC 1921
Db 590 LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluArgLysSer 609
QY 1922 TCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGTCTCTCCATATCTT 1981
Db 610 AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629
QY 1982 ATGGACACTGCAACGAGGGTTCGAGGAGACCGCTGCTTTTGGTGTGCTGGATTAATCT 2041
Db 630 IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla 649

QY 2042 AACTTCTTCCATAGGATAGTACAAAAACAGACGCGGTTTCGCCATTTGAGTGGCGGT 2101
Db 650 AsnPhePheTyrArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGly 669
QY 2102 TATGTCATAGGAGAAACCTCATCTACTTGTTCAGATAGATCTTGTAGTGCATTTTGT 2161
Db 670 TyrAlaLeuGlyIleThrAlaThrThrProAlaGluAspGlnLeuThrPheAlaPheCys 689
QY 2162 CAGCTCTTTGGAGAGATAGAGACTTCTTGTAGCTAAGAATCAAGGTACAGTCTACGGA 2221
Db 690 GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly 709
QY 2222 GGAATCTCTATTACAGACACAAACCAACCTATATCTCTCTCTCTCTCTCTCTCTCT 2275
Db 710 AlaSerLeuTyrPheHisIleThrGlyLeuPheAspIleAlaAsnPheLeuTrpGly 729
QY 2276 -----CGCCCTTGTTCGTTGCTTATGTTCTCTACAGAGATTCCTGTTCTCTTT 2323
Db 730 LysAlaThrArgAlaProTrpValLeuSerGluIleSerGlnIleIleProLeuSerPhe 749
QY 2324 TCAGGAAACCTTAGCTCACCCATACCGATACAGTCTGAAAAACCAAGTATACACATAT 2383
Db 750 AspAlaLysPheSerTyrLeuHisThrAspAsnHisMetLysThrTyrTyrThrAspAsn 769
QY 2384 CTTACTGTTTAAAGGAGCTGGGGATGATAGTTCGCTTTAGATTCGGTGGAGAGCT 2443
Db 770 SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu 789
QY 2444 CCGATTGCTTAGATGAAGTCTCTATTGAGCAGTATACATGCCCTTCATGAAATTCGAG 2503
Db 790 ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln 809
QY 2504 TTTGCTATGCTCATCAGGAAGTTTAAAGAACAGGAAACAGAGCTCGTGAATTCGA 2563
Db 810 TyrIleTyrAlaHisGlnGlnAspPheTyrGluArgHisAlaGluGlyArgAlaPheAsn 829
QY 2564 AGTAGCGCTTGTGAATCTTCTGCTTACCTATCGGGATCCGATTTCGTAAGGAATCAGAC 2623
Db 830 LysSerGluLeuIleAsnValGluIleProIleGlyValThrPheGluArgAspSerLys 849
QY 2624 TGCAAGATGCAACCTCAATTAATCTCTGTTGTTATCTGTTGATCTTGTTCGTAGTAAC 2683
Db 850 SerGlyLysGlyThrTyrAspLeuThrLeuMetTyrIleLeuAspAlaTyrArgArgAsn 869
QY 2684 CCGACTGTACACAACACTCGAATGATGCGGTGATCTTGGAAAAACCTTCGTACGAAT 2743
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QY 2744 TTGGCAAGACAAGCTTTAGTCTCTGTCGAGGGAACCACTTTTGTCTTAACCTCAAAATTT 2803
Db 890 LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlnValAsnProHisMet 909
QY 2804 GAAGCCTTTAGCAATTTCTTTGAAATGCGTGGTGCATCTCGCAATTCAGATGAC 2863
Db 910 GluIlePheGlyGlnPheAlaPheGluValArgSerSerArgAsnTyrAsnThrAsn 929
QY 2864 TTAGGAGCAAAATACCAATTC 2884
Db 930 LeuGlySerLysPheCysPhe 936

RESULT 3

US-10-324-129-3
; Sequence 3, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th-
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01

;; PRIOR APPLICATION NUMBER: US 60/132,272
;; PRIOR FILING DATE: 1999-05-03
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 936
;; TYPE: PRT
;; ORGANISM: Chlamydia pneumoniae
US-10-324-129-3

Alignment Scores:
Pred. No.: 6.38e-153 Length: 936
Score: 1965.00 Matches: 411
Percent Similarity: 62.30% Conservative: 179
Best Local Similarity: 43.40% Mismatches: 327
Query Match: 36.33% Indels: 30
DB: 12 Gaps: 16

US-09-428-122-1 (1-3000) x US-10-324-129-3 (1-936)

QY 101 ATGAAGTCTTCTTCCCAAGTTTGATTTTCTACATTTGCTATTTTC---CCTTTGCTCT 157
Db 1 MetLysSerValSerValSerLeuPhePheSerSerLeuPheSerSerLeuSer 20
QY 158 ATGATTGCTACCGAGACAGATTTTGGATTCAAGT---CGGAGTTTCGATGGAAATAAAT 214
Db 21 IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrAspGlySerAsnGly 40
QY 215 GGTAATTTTTCAGTTTCGTGAGAGCAGGAA---GATGCTGGAATCTACCTACTATTTAAG 271
Db 41 ThrThrPheThrValPheSerThrThrAspAlaAlaAlaGlyThrThrTyrSerLeuLeu 60
QY 272 GGAATGTCACCTAGAAAATATTCTCGAAGCAGGACAGCAATCACAAAAGCTGTTT 331
Db 61 SerAspValSerPheGlnAsnAlaGlyAlaLeuGlyLeuProLeuAlaSerGlyCysPhe 80
QY 332 AACAACTAAGGGGATTTCACTTTTCACAGTACGGGAATCTCTATTGTTCCAAACG 391
Db 81 LeuGluAlaGlyGlyAspLeuThrPheGlnGlyAsnGlnHisAlaLeuLysPheAlaPhe 100
QY 392 GTGGATGACAGGACTGTAGAGGGGCTGCTGTATACAGCAGCGTGTAGATAAATCTACC 451
Db 101 IleAsnAlaGlySerSerAlaGlyThrValAlaSerThrSerAlaAlaAspLysAsnLeu 120
QY 452 ACCTTTATAGGCTTTCTTCGCTATCTTTTATTCGCTCTCCTCGGAAGTTCGATAACT--- 508
Db 121 LeuPheAsnAspPheSerArgLeuSerIleSerCysProSerLeuLeuSerPro 140
QY 509 ACCGGCAAGAGCGGTAGCTGCTACGGGTAGCTTTCAGTTTCACAAAATGTCAGT 568
Db 141 ThrGlyGlnCysAlaLeuLys---SerValGlyAsnLeuSerLeuThrGlyAsnSerGln 159
QY 569 TTGCTCTTCAGCAAAACTTTTCAACGGATATGCGGTGCTATCACCGCAAAACTCTT 628
Db 160 IleIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAsnThrLysAsnPhe 179
QY 629 TCATTAAACAGGACTACATGTCAGCTGTTTTCGAAATACC-----TCCTCAAG 682
Db 180 LeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThrGlyLys 199
QY 683 AAAGCGGAGCCATTACAGCTCCGATGCCCTTACATTTACATTTGGAACCAAGGGGAGTC 742
Db 200 GlnGlyGlyValValThrAlaThrGlyThrIleThrIleGluAsnSerProGlyIleVal 219
QY 743 TCTTTTCTGACAACTTCTTCGGATTCGTGAGCTGCAATTTTACAGAAGCTTCGGTG 802
Db 220 SerPheSerGlnAsnLeuAlaLysGlySerGlyGlyAlaLeuTyrSerThrAspAsnCys 239
QY 803 ACTATTCTTAATAGTCAAGTTTCTTTTATTTGACAATTAAGTTCACAGGAGCGAGTCC 862
Db 240 SerIleThrAspAsnPheGlnValIlePheAspGlyAsnSerAlaTrpGluAlaGln 259
QY 863 TCAACAACGGGGATATGTACAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACT 922

Db 260 Ala-----GlnGlyGlyAlaIleCysCys-----ThrThrThrAspLys 272
QY 923 AAGGTCAACCTCAGTGAATCAGATGTTACTTCTTCAGCAACATACATCAGCAACAGCG 982
Db 273 ThrValThrLeuThrGlyAsnLysAsnLeuSerPheThrAsnAsnThrAlaLeuThrTyr 292
QY 983 GGGGAGCTATCTATGTGAAAGCTCGAACCTGCGTTCGGAGGACTTACCTTATTCAGT 1042
Db 293 GlyGlyAlaIleSerGlyLeuLysValSerIleSerAlaGlyGlyProThrLeuPheGln 312
QY 1043 AGAAATAGTCTCAATCGAGGTACAGCTCCTAAA-----GGTGGAGCCATAGCTATCGAA 1096
Db 313 SerAsn---IleSerGlySerSerAlaGlyGlnGlyGlyGlyAlaIleAsnIleAla 331
QY 1097 GATAGTGGGGAATGATTTATCCGCCGATAGTGGTGACATTTCTTTTATGGGAATACA 1156
Db 332 SerAlaGlyGluLeuAlaLeuSerAlaThrSerGlyAspIleThrPheAsnAsnAsnGln 351
QY 1157 GTCATCTTACTACTCTCTCGGAGCAATAGAGTAGTATGACTTAGAACGAGTGCAGAG 1216
Db 352 ValThrAsnGlySerThrSerThr---ArgAsnAlaIleAsnIleIleAspThrAlaLys 370
QY 1217 ATCAGAGCTTTGCGTCTGCTGTAGAGCCATCTACTTCTTATGATCCCATACATACA 1276
Db 371 ValThrSerIleArgAlaAlaThrGlyGlnSerIleTyrPheTyrAspProIleThrAsn 390
QY 1277 GGTATCCACACAGTTACAGATGCTTAAAGTTAATGAGTATGAGACTCCGGCAGATTCGCA 1336
Db 391 ProGlyThrAlaAlaSerThrAspThrLeuAsnLeuAsnLeuAlaAspAlaAsnSerGlu 410
QY 1337 CTCAATATACAGGACATCATCTTCACAGGAGAAAGTTATCAGAGACAGAGCGCGCA 1396
Db 411 IleGlnTyrGlyAlaIleValPheSerGlyGlnLysLeuSerProThrGluLysAla 430
QY 1397 GATTCTAAAAATCTTACTTCGAAGCTACTCAGCCTGTAATCTTTTCAGGAGGTACTCTA 1456
Db 431 IleAlaAlaAsnValThrSerThrIleArgGlnProAlaValLeuAlaArgGlyAspLeu 450
QY 1457 TCTTTAAACATGAGGTGACTCTCCAGACTCAGCATTCTCAGAGGAGGATTCGCT 1516
Db 451 ValLeuArgAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg 470
QY 1517 CTCGAATGACGCTAGGACATCTACTAGAACCTCTGATACATAGC---ACCATAAACAAAT 1573
Db 471 IleLeuMetAspGlyGlyThrLeuSerAlaLysGluAlaAsnLeuSerLeuAsnGly 490
QY 1574 TTGCTGCTTAAACATCAGTTCTATAGCGGTGCAAGGAGGCAAAATAAGAACCAAGCT 1633
Db 491 LeuAlaValAsnLeuSerSerLeuAspGlyThrAsnLysAlaAlaLeuLysThrGluAla 510
QY 1634 ACGTCAAAAATCTGACTTTATCTGGAACCATCTATTATTTGGACCCGACGCGCTTT 1693
Db 511 AlaAspLysAsnIleSerLeuSerGlyThrIleAlaLeuIleAspThrGluGlySerPhe 530
QY 1694 TATGAAATCATAGTTTAAAGAAATCTCAGTCCTACGACATCTTAGAGCTCAAA----- 1747
Db 531 TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrAla 550
QY 1748 ---GCTTCTGGAACCTGTAACAGCAGCAGCTCCAGATCTCTATATATGGGTGAGAAA 1804
Db 551 GlyAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrLeuGlnProGlu 570
QY 1805 TTCCATTAACGCTATCAGGAACTTGGGGCCCAATTTGTTGGGGACAGGGGCTTCTACG 1864
Db 571 ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
QY 1865 ---ACTGCAACCTTCAACTGAGCTAAAACCTGCTATATTTCTTAATCCGAGGTATCGC 1921
Db 590 LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluArgLysSer 609
QY 1922 TCTTTAGTCCCTTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTATCT 1981

Db	610	AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu	629
QY	1982	ATGAGACTGCAAAACGAAGGGTTGCAGGGAGACCGTCTTTGGTGTGCTGGATTATCT	2041
Db	630	IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla	649
QY	2042	AAC TTCCTTCATTAAGGATAGTACAAAAACAGCAGCGGGTTTCGCATTTCAGTGGCGGT	2101
Db	650	AsnPhePheTyrArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGly	669
QY	2102	TANTGCATACGAGGAACCTACACTCTGTTCAGATAAGATTCTTAGTCGTGCATTTTGT	2161
Db	670	TyrAlaLeuGlyIleThrAlaThrProAlaGluAspGlnLeuThrPheAlaPheCys	689
QY	2162	CAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTACGGA	2221
Db	690	GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly	709
QY	2222	GGAACTCTTATTAACGAGCAACGAAACCTATATCTCTCTCTTCCAACTA-----	2275
Db	710	AlaSerLeuTyrPheHisHisThrGluGlyLeuPheAspIleAlaAsnPheLeuTrpGly	729
QY	2276	-----CGGCCCTGTCTCTCTCTCTTATCTCTACAGAGATTCTCTGTCTCTCTTT	2323
Db	730	LysAlaThrArgAlaProTrpValLeuSerGluLeuSerGlnIleIleProLeuSerPhe	749
QY	2324	TCAGGAAACCTTAGCTACCCATACGGATAACGATCTGAAAAACCAAGTATACAACTAT	2383
Db	750	AspAlaLysPheSerTyrLeuHisThrAspAsnHisMetLysThrTyrThrAspAsn	769
QY	2384	CCTACTGTTAAAGAAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCT	2443
Db	770	SerIleLeuLysGlySerTyrArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu	789
QY	2444	CCGATTTCGTAGATGAAGTCTCTATTGCAGCAGTACATGCCCTTCATGAAATTCGAG	2503
Db	790	ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln	809
QY	2504	TTTGTCTATGCATCATCAGGAAGTTTAAAGAACAGGGAACAGAAAGCTCGTGAATTTGGA	2563
Db	810	TyrIleTyrAlaHisGlnAspPheTyrGluArgHisAlaGluGlyArgAlaPheAsn	829
QY	2564	AGTAGCCGTCTTGTGAATCTTCCTTACCTATCGGATCCGATTGTGATAGGAATTCAGC	2623
Db	830	LysSerGluLeuIleAsnValGluIleProIleGlyValThrPheGluArgAspSerLys	849
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Db	850	SerGluLysGlyThrTyrAspLeuThrLeuMetTyrIleLeuAspAlaTyrArgArgAsn	869
QY	2684	CCGACTGTACGACAACTCGCAATTAGCGGTGATCTTTGGAAAACTTCGGTACGAAT	2743
Db	870	ProLysCysGlnThrSerLeuIleAlaSerAspAlaAsnTrpMetAlaTyrGlyThrAsn	889
QY	2744	TTGGCAACAGACGCTTAGTCTTCGTGCGGGAACCATTTTTCCTTTAACTCAAATTTT	2803
Db	890	LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlnValAsnProHisMet	909
QY	2804	GAAGCCCTTTAGCCAAATTTCTTTTGAAATTCGGTGGTTCATCTCCCAATTAACAAATGAGC	2863
Db	910	GluIlePheGlyGlnPheAlaPheGluValArgSerSerArgSerTyrAsnThrAsn	929
QY	2864	TTAGAGCAAAATACCAATTC 2884	
Db	930	LeuGlySerLysPheCysPhe	936

RESULT, T 4

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RES001 *
US-09-452-380-4
; Sequence 4, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: COHEN, Raymond P.
;
187 GlyLysGlnGlyValValTyAlaThrIleThrIleGluAsnSerProGly 206
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
737 GAAGTCTCTTTTTCACAAATCTTCGGATTCTGGAGCTGCAATTTTACAGAAACC 796
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
207 IleValSerPheSerGlnAsnLeuAlaLysGlySerGlyGlyAlaLeuTySerThrAsp 226
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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; Sequence 4, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-324-129-4

Alignment Scores:
Pred. No.: 2,12e-151      Length: 925
Score: 1946.50             Matches: 404
Percent Similarity: 62.54%   Conservative: 177
Best Local Similarity: 43.49%  Mismatches: 319
Query Match: 35.99%         Indels: 29
DB: 12                      Gaps: 15

US-09-428-122-1 (1-3000) x US-10-324-129-4 (1-925)
Qy 152 TTGCTATGATGCTACCGAGAGAGAGTTGGATTCAAGT---GCGAGTTTCGATGGAAAT 208
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Qy 209 AAAAAATGTAATTTTCAGTTCTGAGAGTCAGGAA---GATGCTCGAATACCTACCTA 265
Db 28 AsnGlyThrThrPheThrValPheSerThrThrAspAlaAlaAlaGlyThrThrTyrSer 47
Qy 266 TTAAAGGGAATGCTACTCTAGAAAATATTCTCGAACAGGAGCAGCAATACAAAAGC 325
Db 48 LeuLeuSerAspValSerPheGlnAsnAlaGlyAlaLeuGlyIleProLeuAlaSerGly 67
Qy 326 TGTTTTAAACAACACTAAGCGGATTCAGTTTACAGGTAAGCGGACTCTCTATTGTC 385
Db 68 CysPheLeuGluAlaGlyAspLeuThrPheGlnGlyAsnGlnHisAlaLeuLysPhe 87
Qy 386 CAAACGGTGAGTACGAGGAGTGTAGCAGGGGCTGCTTTAAACAGCAGCGGTGTAGATA 445
Db 88 AlaPheIleAsnAlaGlySerSerAlaGlyThrValAlaSerThrSerAlaAlaAspLys 107
Qy 446 TCTACACGTTTATAGGTTTCTTCGCTATCTTTTATTCGCTCTCTCGAAGTTCGATA 505
Db 108 AsnLeuLeuPheAsnAspPheSerArgLeuSerIleIleSerCysProSerLeuLeuLeu 127
Qy 506 ACT---ACCGGCAAGGAGCGGTAGTGTCTACGGGTAGCTTGTAGTTTGACMAAAAT 562
Db 128 SerProThrGlyGlnCysAlaLeuLys--SerValGlyAsnLeuSerLeuThrGlyAsn 146
Qy 563 GTCAGTTTGTCTTACGAAAAATCTTTCAACGGATAATAGCGGTGCTATCACCAGCAAA 622
Db 147 SerGlnIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAsnThrLys 166
Qy 623 ACTCTTTTCAATACAGGAGTACAATGTACAGTCTGTTTCTGAAATACC-----TCC 676
Db 167 AsnPheLeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThr 186
Qy 677 TCAAGAAAGCGGAGCGCATTCAGCTTCGATCGCCCTTACCATTAATCTGAAACCAAGGG 736
Db 187 GlyLysGlnGlyValValThrAlaThrGlyThrIleThrIleGluAsnSerProGly 206
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250 GlySerSer-----AspGlyCysGlyGlyAlaIleHisCysSerLysThr 264
QY |||||
911 AGTACAGATACCTAGGTCACCTCAGTGGAAATCAGATGTTACTCTTCAGCAACAATACA 970
Db |||||
265 GlySerAlaProThrLeuThrIleArgAspAsnLysValLeuIlePheGluGluAsnThr 284
QY |||||
971 TCGACACACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTTCGAGGAGCTT 1030
Db |||||
285 SerSerAlaLysGlyGlyAlaIleThrAspLysLeuIleLeuThrSerGlyGlyPro 304
QY |||||
1031 ACCCTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGTGGAGCCATAGCT 1090
Db |||||
305 ThrAlaPheIleAsnAsnLysValThrHisAlaThr---ProLysGlyGlyAlaIleGly 323
QY |||||
1091 ATCGAAGATAGTGGGAATGAGTTATCCCGCATAGTGTGTCGATGTCATGCTTTTAGGG 1150
Db |||||
324 IleAlaAlaAsnGlyGluCysSerLeuThrAlaGluHisGlyAspIleThrPheAspAsn 343
QY |||||
1151 AATCAGTCATCTTACTACTCTCTGGGAGC---AATAGAAGTAGTATCGACTTAGGAACG 1207
Db |||||
344 AsnLeuMetAlaThrGlnAspAsnAlaThrIleLysArgAsnAlaIleAsnIleGluGly 363
QY |||||
1208 AGTCAAAAGATGACAGCTTTTGGTTCTGCTGTGTAGAGCCATCTACTTCTATGATCCC 1267
Db |||||
364 AsnGlyLysPheValAsnLeuArgAlaAlaSerGlyLysThrIleSerPheIleAspPro 383
QY |||||
1268 ATAACTCAGGATCATCCACACAGTGTACAGTGTCTTAAAGTTAATCAGACTCCGCA 1327
Db |||||
384 IleThrValGluGlyAsn-----AlaAlaAspLeuLeuThrLeuAsnLysAlaGluGly 401
QY |||||
1328 GATTCGCACTACATATACAGGGAACATCATCTTCACAGGAGAAAGTTATCAGAGACA 1387
Db |||||
402 AspLysThr-----TyrAsnGlyArgIleIlePheSerGlyLysLeuThrGluGlu 419
QY |||||
1388 GAGGCGCGAGATCTTAAATACTTACTTCTGAAAGTCTACAGCTGTAACTCTTTCAGGA 1447
Db |||||
420 GlnAlaAlaValAlaAspAsnLysThrThrPheThrGlnProIleThrLeuAlaAla 439
QY |||||
1448 GGTACTCTTACTTTAAACATCGAGTGTCTGCGAGCTCAGGATCTACTCAACAGGCA 1507
Db |||||
440 GlyGluLeuValLeuArgSerGlyValGluValGluAlaLysThrValValGlnThrAla 459
QY |||||
1508 GATTCCTCGTCTCGAATGGAGCTAGGAATCTACTCTAGAA---CCTGCTGATAGTACAC 1564
Db |||||
460 GlySerLeuIleLeuMetAspAlaGlyThrLysLeuSerAlaLysThrGluAspAlaThr 479
QY |||||
1565 ATAAACATTTGGTCTATTAAACATCATCTTCTATAGAGCGGTGCAAGAGCAAAATAGAA 1624
Db |||||
480 LeuThrAsnLeuAlaIleAsnProAsnThrLeuAspGlyLysLysPheAlaValAsp 499
QY |||||
1625 ACCAAAGCTACGTCAAAAATCTGACTTTTATCTGGAACCATCTATCTTATGACCCGAGC 1684
Db |||||
500 AlaValAlaAlaGlyLysAsnValThrLeuSerGlyAlaIleGlyValIleAspProThr 519
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RESULT 7

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US-10-023-437-57
; Sequence 57, Application US/10023437
; Publication No. US20020183272A1
GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; PRIORITY FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIORITY FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-57

Alignment Scores:
Pred. No.: 8,3e-149 Length: 926
Score: 1915.00 Matches: 410
Percent Similarity: 59.27% Conservative: 156
Best Local Similarity: 42.93% Mismatches: 333
Query Match: 35.40% Indels: 56
Gaps: 18

US-09-428-122-1 (1-3000) x US-10-023-437-57 (1-926)
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QY 101 ATGAAGTCTCTTCCCAAGTTTGTTATTTTCTACATTTGCTATTTTCCCTTTGTCTATG 160
Db |||||
1 MetArgProSerLeuTyrLysIleLeuIleSerSerThrLeuThrLeuProIleSerPhe 20
QY 161 -----ATTGTCACGAGACAGTTTTGGATTCAAGT 190
Db |||||
21 HisPheSerGlnLeuHisAlaGluValAlaLeuThrGlnGluSerIleLeuAspAla--- 39
QY 191 GCGAGTTTCGATGGGAATAAATGTTATTTTTCAGTTTCGTGAGAGTCAGGAGATGCT 250
Db |||||
40 -----AsnGlyAlaPheSerProGlnSerThrSerThrAlaGly 52
QY 251 GGAACCTACCTACTTAAAGGGAATGTCACTCTAGAAAATATTCCTGGAAACAGGCACA 310
Db |||||
53 GlyThrIleTyrAsnValGluSerAspIleSerIleValAspVal---GlyGlnThrAla 71
QY 311 GCAATCACAAAAGCTGTTTAAACACACTAAGGCGATTGCTTTCAGGTACAGTACGGG 370
Db |||||
72 AlaLeuAlaSerSerAlaPheValGlnThrAlaAspAsnLeuThrPheLysGlyAsnAsn 91
QY 371 AACTCTCTATTGTTCCAAACGGTGGATGAGGAGCTGTAGCAGGGCTGCTGTTAACAGC 430
Db |||||
92 HisSerLeuSerIleThrAsnAlaAsnAlaGly---AlaAsnProAlaGlyIleAsnVal 110
QY 431 AGCGTGTAGATAAATCTACCAAGTTTATAGGGTTTCTTCGCTATCTTTTATTGCGTCT 490
Db |||||
111 AsnThrAlaAspLysIleLeuThrLeuThrAspPheSerLysLeuSerPheLysGluCys 130
QY 491 CTTGGAAGTTTCGATAACTACCGCAAGAGCGGTAGCTGCTCTACGGGTAGCTTGAGT 550
Db |||||
131 ProSerSerLeuValAsnThrGlyLysGlyAlaMetLys---SerGlyGlyAlaLeuAsn 149
QY 551 TTGACAAAATGTCAGTTTCTCTTCAGCAAAACTTTTCAACGGGATAATGCGGTGCT 610
Db |||||
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QY	2720	TCTTGGAAAACCTTCGGTAGCAATTTGGCAAGACAGCTTTAGTCTCCTTCGTGCGAGGGAAC	2779
Db	872	SerTrpLeuThrThrAlaThrAsnLeuAlaArgGlnAlaPheIleValArgAlaGlyAsn	891
QY	2780	CATTTTTCCTTAACTCAAATTTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGTGGG	2839
Db	892	HisIleAlaLeuThrSerGlyValGluMetPheSerGlnPheGlyPheGluLeuArgSer	911
QY	2840	TCATCTCGCAATTAACAATGTAGACTTTAGAGAGCAAAATACCAATTC	2884
Db	912	SerSerArgAsnTyrAsnValAspLeuGlyAlaLysValAlaPhe	926

RESULT 8
US-09-738-269-23
; Sequence 23, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALPENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-23

Alignment Scores:
Pred. No.: 8,64e-128 Length: 839
Score: 1659.50 Matches: 384
Percent Similarity: 54.17% Conservative: 287
Best Local Similarity: 40.00% Mismatches: 287
Query Match: 30.68% Indels: 153
DB: 12 Gaps: 25

US-09-428-122-1 (1-3000) x US-09-738-269-23 (1-839)

QY	89	ATATATTTTACAAAGTCTCTTCCCAAGTTGTATTTCTACATTTTCTATTTC	148
Db	5	ValTyrTrpPheLeuIleSerSer-----SerLeuPheAlaSerAsn	18
QY	149	CCTTTGTCTATGATT---GCTACCGAGACAGTTTTCGATTCGAAGTCGCGAGTTTCGATGGG	205
Db	19	SerLeuSerPheAlaAsnAspAlaGlnThrAlaLeuThrProSerAspSerTyrAsnGly	38
QY	206	AAT---AAAAATGTTAATTTTCAGTTCGTCGAGAGTCAGAGAGATGCTGGAACTACCTAC	262
Db	39	AsnValThrSerGluGluPheGlnValLysGluThr-----SerSerGlyThrThrTyr	56
QY	263	CTATTTAAGGAAATGTCACTCTAGAAAATATTCTCTGGACACGACGACATCACAAAA	322
Db	57	ThrCysGluGlyAsnValCysIle---SerPheAlaGlyLysAspSerGlyLeuLysLys	75
QY	323	AGCTGTTTTACACAACTTAAGGGCGATTTCGACTTCACAGGTAAACGGGAACCTCTATTG	382
Db	76	SerCysPheSerAlaThr---AspAsnLeuThrPheLeuGlyAsnGlyTyrThrLeuCys	94
QY	383	TTCCAAAACGGTGGATGACGGGACTGTAGCAGGGGCTGTGTTAAACAGCAGCGTGTAGAT	442
Db	95	PheAspAsnIleThrThrThrAlaSerAsnProGlyAlaIleAsnValGlnGlyGlnGly	114
QY	443	AAATCTACACGTTTATAGGTTTTCTTCGCTATCTTTTATTCGGTCTCCTCGGAAGTTCG	502
Db	115	LysThrLeuGlyIleSerGlyPheSerLeuPheSerCysAlaTyrCysProGly---	133

503	ATAACTACCGGCAAGGAGCGCTTAGCTGCTCTACTACGGTAGCTTGAGTTTGACAAAAAT	562	QY
134	--ThrThrGlyTyrGlyAlaileGln--ThrLysGlyAsnThrThrLeuLysAspAsn	151	Db
563	GTCAGTTTGCTCTTCAGCAAAAACTTTTCACGGATAATGCGGTGCTTATCACCGCAAAA	622	QY
152	SerSerLeuValPheHisLysAsnCysSerThrAlaGluGlyGlyAlaileGlnCys---	170	Db
623	ACTCTTTTCATTAAACAGGGACTACAATGTCAGCTCTGTTTCTGTGAAAATACCTCTCAAAG	682	QY
170	-----	170	Db
683	AAAGCGGAGCCATTTCAGACTTCCGATGCCCTTACATTACTTGGAAACCAAGGGGAAGTC	742	QY
170	-----	170	Db
743	TCCTTTTCTGACANTACTTCTTCGGATCTCGAGCTGCAATTTTACAGAAGCCTCGGTG	802	QY
170	-----	170	Db
803	ACTATTTCATAATAAGTTTCCTTTATTGACATAAGTACAGGAGCGAGCTCC	862	QY
170	-----	170	Db
863	TCAACAACGGGGGATATGTCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATCT	922	QY
171	-----LysGlySerSerAspAla	176	Db
923	AAGTCCACCTCCTCTGGAANTCAGATGTTACTCTTCAGCAACAATACATCGACACAGCG	982	QY
177	GluLeuLysIleGluAsnAsnGlnAsnLeuValPheSerGluAsnSerSerThrSerLys	196	Db
983	GGAGGAGCTATCTATCTGAAAAAGCTCGAATGGCTTCGGGAGGACTTACCTTATTCAGT	1042	QY
197	GlyGlyAlaIleTyrAlaAspLysLeuThrIleValSerGlyGlyProThrLeuPheSer	216	Db
1043	AGAAATAGTGTCAATCGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATCGAAGAT---	1099	QY
217	AsnAsnSerValSerAsnGlySerSerProLysGlyGlyAlaIleSerIleLysAspSer	236	Db
1100	AGTGGGGAATGAGTTATCCGCGGATAGGTGACATTGTCTTTTAGGGATACAGTC	1159	QY
237	SerGlyGlyCysSerLeuThrAlaAspLeuGlyAspIleThrPheAspGlyAsnLysIle	256	Db
1160	ACTTCTACTACTCTCTGGAGCGAAT-----AGAACTAGTATCGACTTAGGAACGAGT	1210	QY
257	IleLysThrSerGlyGlySerSerThrValThrArgAsnSerIleAspLeuGlyThr---	275	Db
1211	GCAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGACCATCTACTTCTATGATCCCAT	1270	QY
276	GlyLysPheThrLysLeuArgAlaLysAspGlyPheGlyIlePhePheTyrAspProIle	295	Db
1271	ACTACAGGATCATCCACAACAGTTTACAGATGTCTTAAAGCTTAATGAGACTCCGGCAGAT	1330	QY
296	ThrGlyGlyGlySer-----AspGluLeuAsnIleAsnLys-----Lys	308	Db
1331	TCCTGCATCAATATACAGGAAACATCATCTTCACAGAGAAAAAGTTTATCAGAGACAGAG	1390	QY
309	GluThrValAspTyrThrGlyLysIleValPheSerGlyGluLysLeuSerAspGluGlu	328	Db
1391	GCCGCGAATTCATAAAATCTTACTTCGAAGCTACTACAGCTGTAACTCTTTTCAGAGGT	1450	QY
329	LysAlaArgAlaGluAsnLeuAlaSerThrPheAsnGlnProIleThrLeuSerAlaGly	348	Db
1451	ACTCTATCTTTAAACATGAGTGAACCTCTCGCAGACTCAGGCATTCATCAACAGGCAGAT	1510	QY
349	SerLeuValLeuLysAspGlyValSerValThrAlaLysGlnValThrGlnGluAlaGly	368	Db
1511	TCTCGTCTCGAAATGGAGGTAGGAACCTCTAGAACT-----GCTGATACT	1558	QY
369	SerThrValValMetAspLeuGlyThrThrLeuGlnThrProSerSerGlyGlyGluThr	388	Db
1559	AGCACCAATAACAATTTGGTCAATTAACATCATGTTCTATA-----GACGGTGCAAG	1609	QY

Db	389	IleThrLeuThrAsnLeuAspIleAsnIleAlaSerLeuGlyGlyGlyThrSer	408
Qy	1610	AAGCGAAATAAGAACCAAGCTACGTCACAAATACTGACTTTATCTGGAACCACTACT	1669
Db	409	ProAlaLysLeuAlaThrAsnThrAlaSerGlnAlaIleThrIleAsn--AlaValAsn	427
Qy	1670	TTATGGACCCGACGGGACGTTTATGAAATCATAGTTTAAAGAAATCCCTCAGTCTAC	1729
Db	428	LeuValAspAlaAspGlyAsnAlaTyrGluAspProIleLeuAlaThrSerLysProPhe	447
Qy	1730	GACATCTTAGAGCTCAAAGCTTCTGGAAGCTTAAACAAGCAGCGCAGTGCATCCAGATCCT	1789
Db	448	ThrAlaIle-----ValAlaThrThrAsnAlaSerThrValThrGlnProThrAsp	464
Qy	1790	ATAATGGGTGAG-----AAATTCCATTACGGCTATCAGGGAACATTGGGGCCCAATT	1840
Db	465	AsnLeuThrAsnTyrValProProThrHisTyrGlyTyrGlnGlyAsnTrp--ThrVal	483
Qy	1841	GTTTGGGGACACGGGCTCTTAGC---ACTGCAACCTTCAACTGCAGTAAAACTGGCTAT	1899
Db	484	ThrTrpAspThrGluThrAlaThrLysThrAlaThrLeuThrTrpGluGlnThrGlyTyr	503
Qy	1898	ATTCTTAATCCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATCGATTATA	1957
Db	504	SerProAsnProGluArgGlnGlyProLeuValProAsnThrLeuTrpGlyAlaPheSer	523
Qy	1958	GATPATTAGCTCTCTCATTTATCTTATGGAGACTGCAACAGAGGGTTGCAGGAGACCGT	2017
Db	524	AspLeuArgAlaIleGlnAsnLeuMetAspIleSerValAsnGlyAlaAspTyrHisArg	543
Qy	2018	GCATTTGGTGCTCGATTACTACTTCTTCCATAAGATAGTACAAACACGACCC	2077
Db	544	GlyPheTrpValSerGlyLeuAlaAsnPheLeuHisLysSerGlySerAspThrLysArg	563
Qy	2078	GGGTTTCGCCATTGTAGTGGCGGTATGTATAGGAGAGAAACCTACATACTTGTTCAGAT	2137
Db	564	LysPheArgHisAsnSerAlaGlyTyrAlaLeuGlyValTyrAlaLysThrProSerAsp	583
Qy	2138	AAGATCTTATAGTGTGCATTTTGTACGCTCTTTGGAGAGATAGAGACTACTTTGTAGCT	2197
Db	584	AspIlePheSerAlaAlaPheCysGlnLeuPheGlyLysAspLysAspTyrLeuValSer	603
Qy	2198	AAGATCAAGGTACAGTCTACGGAGGAACTCTCTTATCCAGACACACGAACTATATC	2257
Db	604	LysAsnAsnAlaAsnIleTyrAlaGlySerLeuTyrTyrGlnHis-----Ile	619
Qy	2258	TCCTCTCTTGCAAACTACGGCCTTGTTCGTTCTTATGCTTCTCCTACAGAGATTCCTGTT	2317
Db	620	SerTyrTrpSerAlaTrpGlnAsnLeuLeuGlnAsnThrIleGlyAlaGluAlaProLeu	639
Qy	2318	CTCTTTTCAGGAACCTTAGCTACACCCATACGGATAACGATCTGAAACC-----	2368
Db	640	ValLeuAsnAlaGlnLeuThrTyrCysHisAlaSerAsnAspMetLysThrAsnMetThr	659
Qy	2369	-----AAGTATACACATATCTCTTAAAGAGACCTGGGGAATGAT	2413
Db	660	ThrThrTyrAlaProArgLysThrThrTyrAlaGluIleLysGlyAspTrpGlyAsnAsp	679
Qy	2414	AGTTTCGCTTTAGAAATTCGGTGGGAAGCTCCGATTTGCTTAGATGAAGTGCCTATTT	2473
Db	680	CysPheGlyValGluLeuGlyAlaThrValProIleGlnThrGluSerSerLeuLeuPhe	699
Qy	2474	GAGCAGTACATGCCCTTCATGAATTCGAGTTGTCTATGCATCAGGAGGTTTAA	2533
Db	700	AspMetTyrSerProPheLeuLysPheGlnLeuValHisThrHisGlnAspPheLys	719
Qy	2534	GAAACAGGGAACA-----GAAGCTCGTGAATTTGGAGTAGTACCGCTCTTGATCTTCGCTTA	2590
Db	720	GluAsnAsnSerAspGlnGlyArgTyrPheGluSerSerAsnLeuThrAsnLeuSerLeu	739
Qy	2591	CCTATCGGGATCCGATTGTAAAGGAATCAGACTGCCAAGATGCAACGTACAATCTAACT	2650

Db 740 ProIleGlyLeuIlePheGluArgPheAlaAsnAspThrAlaSerTyrHisValThr 759
 QY 2651 CTTGGTATTACTGTGGATCTTTCGTAGTAACCCGCTGTACGACAACTCGGAATT 2710
 Db 760 AlaAlaTyrSerProAspValArgSerAsnProAspCysThrThrSerLeuLeuVal 779
 QY 2711 AGCGGTGATTCT-----TGGAAACCTTCGGTAGCAATTTGGCAAGCAAGCTTTAGTC 2764
 Db 780 SerProAspSerAlaValTyrValThrLysAlaAsnAsnLeuAlaArgSerAlaPheMet 799
 QY 2765 CTTCTGGCGAGGAACCAATTTTTCCTTAACCTCAATTTTGAAGCCTTTAGCAATTTCT 2824
 Db 800 LeuGlnAlaGlyAsnTyrLeuSerHisAsnIleGluIlePheSerGlnPheGly 819
 QY 2825 TTTGAATTCGGTGGTCATCTCGCAATTAACATGTAGACTTAGGAGCAAAATACCAATTC 2884
 Db 820 PheGluLeuArgGlySerSerArgThrThrAsnValAspLeuGlySerLysIleGlnPhe 839

RESULT 9

US-10-023-437-23
 ; Sequence 23, Application US/10023437
 ; Publication No. US20020183272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHNSTON, STEPHEN A.
 ; APPLICANT: STEMKE-HALE, KATHERINE
 ; APPLICANT: SYKES, KATHRYN F.
 ; APPLICANT: KALTENBOECK, BERNHARD
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS for Vaccination COMPRISING NUCLEIC ACID
 ; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
 ; FILE REFERENCE: UTSD-736US
 ; CURRENT APPLICATION NUMBER: US/10/023,437
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: 60/225,839
 ; PRIOR FILING DATE: 2000-12-15
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 839
 ; TYPE: PRT
 ; ORGANISM: Chlamydia psittaci
 US-10-023-437-23

Alignment Scores:
 Pred. No.: 8,64e-128 Length: 839
 Score: 1659.50 Matches: 384
 Percent Similarity: 54.17% Conservativeness: 136
 Best Local Similarity: 40.00% Mismatches: 287
 Query Match: 30.68% Indels: 153
 DB: 14 Gaps: 25

US-09-428-122-1 (1-3000) x US-10-023-437-23 (1-839)

QY 89 ATATATTTTCAATGAAGTCTCTTCCCAAGTTGTATTTCATATTGCTATTTC 148
 Db 5 ValTyrTrpPheLeuIleSerSer-----SerLeuPheAlaSerAsn 18
 QY 149 CTTTGTCTATGATT---GCTACCGACACAGTTTTCGATTTCAGTCCGAGTTTCGATGG 205
 Db 19 SerLeuSerPheAlaAsnAspAlaGlnThrAlaLeuThrProSerAspSerTyrAsnGly 38
 QY 206 AAT---AAAAATGGTAATTTTTCAGTTTCGTGAGAGTCAGGAAGATCTGGAACCTACTAC 262
 Db 39 AsnValThrSerGluGluPheGlnValLysGluThr-----SerSerGlyThrThrTyr 56
 QY 263 CTATTTAAGGGAATGTCATCTAGAAAATATTCCTGGACAGGCACAGCAATCAAAA 322
 Db 57 ThrCysGluGlyAsnValCysIle---SerPheAlaGlyLysAspSerGlyLeuLysLys 75
 QY 323 AGCTGTTTTTACACACTAAGGGGATTTGACTTTTTCACAGGTAAACGGGAACCTCTCTATTG 382
 Db 76 SerCysPheSerAlaThr---AspAsnLeuThrPheLeuGlyAsnGlyTyrThrLeuCys 94
 QY 383 TTCAAACGGTGGATGCAGGAGCTGTAGCAGGGGCTGCTGTTAAACAGCAGCTGGTAGAT 442

Db 95 PheAspAsnIleThrThrThrAlaSerAsnProGlyAlaIleAsnValGlnGlyGlnGly 114
 QY 443 AAATCTACACAGTTTATAGGGTTTCTCGCTATCTTTTATTCGCTCTCTCGGAAGTTTCG 502
 Db 115 LysThrLeuGlyLysSerGlyPheSerLeuPheSerCysAlaTyrCysProGly--- 133
 QY 503 ATAATCTACCGGCAAAAGAGCCGTAGCTGCTCTCGGGGTAGCTTGAGTTTTCACAAAAAT 562
 Db 134 ---ThrThrGlyTyrGlyAlaIleGln---ThrLysGlyAsnThrThrLeuLysAspAsn 151
 QY 563 GTCAAGTTTCTCTTACGCAAAAACCTTTTCAACGGATATGCGGGTCTATCACGCCAAAA 622
 Db 152 SerSerLeuValPheHisLysAsnCysSerThrAlaGluGlyGlyAlaIleGlnCys--- 170
 QY 623 ACTCTTTTCATTAAACAGGAGTACAATGTCTGCTCTGTTTCTGAAAAATACCTCTCAAG 682
 Db 170 ----- 170
 QY 683 AAAGCGGAGCCATTACAGACTTCCGATGCCCTTACCATTTGGAACCAAGGGAAGTC 742
 Db 170 ----- 170
 QY 743 TCTTTTCTGACAATCTTCTTCGGATTCTGAGCTGCAATTTTACAGAAAGCTCGGTG 802
 Db 170 ----- 170
 QY 803 ACTATTTCTAATAATCTAAAGTTTCTTTTATTGACAATAAGTACAGGAGCAGCTCC 862
 Db 170 ----- 170
 QY 863 TCAACAACGGGGATATGTCTGAGGTGCTATCTGTGCTTATAAACTAGTACAGTACT 922
 Db 171 -----LysGlySerSerAspAla 176
 QY 923 AAGTCAACCTCAGTGAATCAGATGTTACTCTTCAGCAACAATACATCGCAACAGCG 982
 Db 177 GluLeuLysIleGluAsnAsnGlnAsnLeuValPheSerGluAsnSerSerThrSerLys 196
 QY 983 GGAGGAGCTATCTATGTGAAAAAGCTCGAAGCTGCGGTTCGGAGGACTTACCTTATTCAGT 1042
 Db 197 GlyGlyAlaIleTyrAlaAspLysLeuThrIleValSerGlyGlyProThrLeuPheSer 216
 QY 1043 AGAAATAGTCTCAATGGAGTACAGCTCTTAAGGTGGAGCCATGCTATCGAAGAT--- 1099
 Db 217 AsnAsnSerValSerAsnGlySerSerProLysGlyGlyAlaIleSerIleLysAspSer 236
 QY 1100 AGTGGGAATTTGATTTATCCCGCATAGTGGTGCATTTGTTTGGGAATACAGTC 1159
 Db 237 SerGlyGluCysSerLeuThrAlaAspLeuGlyAspIleThrPheAspGlyAsnLysIle 256
 QY 1160 ACTTCTACTACTCTCTGGGCGAAT-----AGAAAGTAGTATCCACTTAGGAAGCT 1210
 Db 257 IleLysThrSerGlyGlySerSerThrValThrArgAsnSerIleAspLeuGlyThr--- 275
 QY 1211 GCAAAGATGACAGCTTTGCTTCTGCTGTGGTAGCCATCTACTTATGATCCATA 1270
 Db 276 GlyLysPheThrLysLeuArgAlaLysAspGlyPheGlyIlePhePheThrAspProIle 295
 QY 1271 ACTACAGATCATCCACACAGTACAGATGCTTTAAAGTTAATGAGATCCGCGCAGAT 1330
 Db 296 ThrGlyGlyGlySer-----AspGluLeuAsnIleAsnLys-----Lys 308
 QY 1331 TCTGCACTACAATATACAGGGAACATCTCTTACAGGAGAAAGTTATCAGACAGACAG 1390
 Db 309 GluThrValAspTyrThrGlyLysIleValPheSerGlyGlyLysLeuSerAspGluGlu 328
 QY 1391 GCCGCAATTTCTAAATCTTACTTCTGAGCTACTACAGCTCTACTCTTTCAGAGGT 1450
 Db 329 LysAlaArgAlaGluAsnLeuAlaSerThrPheAsnGlnProIleThrLeuSerAlaGly 348
 QY 1451 ACTCTATCTTTAAACATGAGTGCAGTCTCTGCACTCAGGACTTCACTCAACAGGCGAGAT 1510

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Db 349 SerLeuValLeuLysAspGlyValSerValThrAlaLysGlnValThrGlnGluAlaGly 368
QY 1511 TCTCGTCTCGAATGACGTAGCACTACTCTAGAACCT-----GCTGATACT 1558
Db 369 SerThrValValMetAspLeuGlyThrThrLeuGlnThrProSerSerGlyGlyGluThr 388
QY 1559 AGCACCATAACAATTTGGTCATTAACATCAGTCTTATA-----GACGGTGCAGAG 1609
Db 389 IleThrLeuThrAsnLeuAspIleAsnIleAlaSerLeuGlyGlyGlyThrSer 408
QY 1610 AAGCAAAATAGAAACCAAGCTACGTCAAAAATCTGACTTATCTGGAACCATCACT 1669
Db 409 ProAlaLysLeuAlaThrAsnThrAlaSerGlnAlaIleThrIleAsn---AlaValAsn 427
QY 1670 TTATTGGACCGGACGGCTTTTAAAGAAATCATAGTTTAAAGAAATCTCAGTCTCTAC 1729
Db 428 LeuValAspAlaAspGlyAsnAlaTyrGluAspProIleLeuAlaThrSerLysProPhe 447
QY 1730 GACATCTTAGAGTCAAAAGCTCTGGAACTGTAAACAGCACCGGAGTACTCCAGATCCT 1789
Db 448 ThrAlaIle-----ValAlaThrThrAsnAlaSerThrValThrGlnProThrAsp 464
QY 1790 ATAATGGGTGAG-----AAATTCATTACGGCTATCAGGGAACCTTGGGGCCCAATT 1840
Db 465 AsnLeuThrAsnTyrValProProThrHisTyrGlyThrGlnGlyAsnTrp---ThrVal 483
QY 1841 GTTTGGGGGACAGGGCTTCTACG---ACTGCAACCTTCAACTGGACTAAACCTGGCTAT 1897
Db 484 ThrTrpAspThrGluThrAlaThrLysThrAlaThrLeuThrTrpGluGlnThrGlyTyr 503
QY 1898 ATTCTTAATCCGAGGTATCGGCTCTTATAGTCTTAATAGTCTTATGGAATGCAATTTATA 1957
Db 504 SerProAsnProGluArgGlnGlyProLeuValProAsnThrLeuTrpGlyAlaPheSer 523
QY 1958 GATATTAGCTCTCCATTATCTTATGAGACTCAAAACGAAGGTTTCAGGGAGACCGT 2017
Db 524 AspLeuArgAlaIleGlnAsnLeuMetAspIleSerValAsnGlyAlaAspTyrHisArg 543
QY 2018 GCTTTTGGTGTGCTGGATCTCTAAGTCTTCCATTAAGGATAGTACAAAACACGACGC 2077
Db 544 GlyPheIrpValSerGlyLeuAlaAsnPheLeuHisLysSerGlySerAspThrLysArg 563
QY 2078 GGGTTTCGCCATTTCAGTGGCGGTATGCTATAGAGAAACCTACATCTTGTTCAGAT 2137
Db 564 LysPheArgHisAsnSerAlaGlyTyrAlaLeuGlyValTyrAlaLysThrProSerAsp 583
QY 2138 AAGATTCTTAGTCTGCATTTTGCAGCTCTTGGAGAGATAGAGACTACTTGTAGCT 2197
Db 584 AspIlePheSerAlaAlaPheCysGlnLeuPheGlyLysAspLysAspTyrLeuValSer 603
QY 2198 AAGATCAAGGTACAGTCTACGGAGAACTCTCTATTACCAGCACACGAAACCTATATC 2257
Db 604 LysAsnAsnAlaAsnIleTyrAlaGlySerLeuTyrTyrGlnHis-----Ile 619
QY 2258 TCTCTCTCCGCAACTACGGCTTGTCTGTTTGTCTTATGTTCTCAGAGATTCCTGTT 2317
Db 620 SerTyrTrpSerAlaTrpGlnAsnLeuGlnAsnThrIleGlyAlaGluAlaProLeu 639
QY 2318 CTCCTTTTCAGGAACTTAGTACACCATACGGATACGATCTCGAAACCC----- 2368
Db 640 ValLeuAsnAlaGlnLeuThrTyrCysHisAlaSerAsnAspMetLysThrAsnMetThr 659
QY 2369 -----AAGTATACACATATCTCTGTTTAAAGGAAGCTGGGGGAATGAT 2413
Db 660 ThrThrTyrAlaProArgLysThrThrTyrAlaGluIleLysGlyAspTrpGlyAsnAsp 679
QY 2414 AGTTTCGCTTGAATTCGGTGGAGAGCTCCGATTTGCTTAGATGAAGTCTCTATT 2473
Db 680 CysPheGlyValGluLeuGlyAlaThrValProIleGlnThrGluSerSerLeuLeuPhe 699
QY 2474 GAGCAGTACATCCCTTCATGAATTCAGTTTGTCTATGTCATCAGGAAGGTTTAAA 2533
Db 700 AspMetTyrSerProPheLeuLysPheGlnLeuValHisThrHisGlnAspAspPheLys 719
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QY 2534 GAACAGGGACACA---GAAGCTCGTGAATTTGGAACTAGCGCTTGTGAATCTTGCCTTA 2590
Db 720 GluAsnAsnSerAspGlnGlyArgTyrPheGluSerSerAsnLeuThrAsnLeuSerLeu 739
QY 2591 CTTATCGGATCCGATTTGATAGGAATCAGACTGCCAAGATGCCAAGATGCAACCTTAAT 2650
Db 740 ProIleGlyIleLysPheGluArgPheAlaAsnAsnAspThrAlaSerTyrHisValThr 759
QY 2651 CTTGGTTATPACTGTGGATCTTGTTCGTAGTAACCCGACTGTACGACACACTGCGAAT 2710
Db 760 AlaAlaTyrSerProAspIleValArgSerAsnProAspCysThrThrSerLeuLeuVal 779
QY 2711 ACGCGTGATCTCT-----TGGAAACCTTCGGTACGAATTTGCAAGACAAAGCTTTAGTC 2764
Db 780 SerProAspSerAlaValTrpValThrLysAlaAsnAsnLeuAlaArgSerAlaPheMet 799
QY 2765 CTTGCGTCAGGGAACCATTTTTCCTTAACTCAAATTTTGAAGCCTTTAGCCAATTTTCT 2824
Db 800 LeuGlnAlaGlyAsnTyrLeuSerLeuSerHisAsnIleGluIlePheSerGlnPheGly 819
QY 2825 TTTGAATTCGGTGGTGCATCTCCCAATTTACAATGTAGACTTAGGACGACAAATACCAATTC 2884
Db 820 PheGluLeuArgGlySerSerArgThrTyrAsnValAspLeuGlySerLysIleGlnPhe 839
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RESULT 10

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US-09-886-468-19
; Sequence 19, Application US/09886468
; Patent No. US20020037293A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pasteur Limited
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th
; FILE REFERENCE: 77813-5
; CURRENT APPLICATION NUMBER: US/09/886,468
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,280
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,281
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,282
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,283
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,284
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,285
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,385
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114,050
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,056
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,057
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,058
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,059
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,061
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-886-468-19
Alignment Scores:
Pred. No.: 1.67e-109 Length: 922
Score: 1437.50 Matches: 350
Percent Similarity: 53.21% Conservative: 156
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Best Local Similarity:	36.80%	Mismatches:	382
Query Match:	26.58%	Indels:	63
DB:	9	Gaps:	26
US-09-428-122-1 (1-3000) x US-09-886-468-19 (1-922)			
QY	113	TTCCCC---AAGTTTGTATTTCTACATTTGCTATTTCCCTTTGCTATGATGCTACC	169
DB	8	PheProLeuValPheSerPheThrLeuLeuSerValPheAspThrSerLeuSerAlaThr	27
QY	170	GAGACATTTTGGATTCACAGTCGAGTTTCGATTCGATGGGAATAAAATGGTAATTTTCAGTT	229
DB	28	ThrIleSerLeuThrProGluAspSerPheHisGlyAspSerGlnAsn-----AlaGlu	45
QY	230	CGTGAGAGTCAGGAAGTCTGGAATCTACCTACTATTAAAGGAAATGCTCACTAGAA	289
DB	46	ArgSerTyrAsnValGlnAlaGlyAspValTyrSerLeuThrGlyAspValSerIleSer	65
QY	290	AATATTCCTGGAACAGGCACAGCAATACAAAGAGTGTTTTAAACAACTAAGGCGGAT	349
DB	66	AsnVal-----AspAsnSerAlaLeuAsnLysAlaCysPheAsnValThrSerGlySer	83
QY	350	TTGACTTCACAGTAACGGAACTCTCTATTCTTCCAAACGCTGGATCGAGGACTGA	409
DB	84	ValThrPheAlaGlyAsnHisGlyLeuTyrPheAsnAsnIleSerSerGlyThrThr	103
QY	410	GCAGGCGCTGCTGTTAACAGCAGCGGTGTAGATAAATCTACCACG---TTTATAGGGTTT	466
DB	104	LysGluGlyAlaValLeuCysCysGlnAspProGlnAlaThrAlaArgPheSerGlyPhe	123
QY	467	TCTTCGCTATCTTTTATTCGCTCTCTCGAAGTTCGATACCTACCGCAAGAGCCGTT	526
DB	124	SerThrLeuSerPheIleGlnSerProGlyAspIleLysGluGlnGly-----	139
QY	527	AGCTGC-----TCTACGGGTAGCTTCAGTTTCACAAAAATGCTCAGTTTGTCTTCACG	580
DB	140	--CysLeuTyrSerLysAsnAlaLeuMetLeuLeuAsnAsnTyrValValargPheGlu	158
QY	581	AAAACTTTTCAACGGNAATGCGGTGCTATCACCGCAAAACTCTTTCATTAAACAGGG	640
DB	159	GlnAsnGlnSerLysThrLysGlyGlyValaIleSerGlyAlaAsnValThrIleValGly	178
QY	641	ACTACATGTCAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTCAG	700
DB	179	AsnTyrAspSerValSerPheTyrGlnAsnAlaAlaThr---PheGlyAlaIleHis	197
QY	701	ACTTCCGATGCCCTTACCATCTACGAAACCAAGGGGAGTCTCTTTTCTGCAATACT	760
DB	198	SerSerGlyProLeuGlnIleAlaValAsnGlnAlaGluIleArgPheAlaGlnAsnThr	217
QY	761	TCITTCGGAT---TCTGGAGCTGCAATTTTACAGACGCTCGTGACTATTTCTAATAAT	817
DB	218	AlaLysAsnGlySerGlyAlaLeuTyrSerAspGlyAspIleAspIleAspGlnAsn	237
QY	818	GCTAAAGTTTCTTTTATTCACATAAGGTCACAGGAGCGAGCTCCTCAACACGGGGAT	877
DB	238	AlaTyrValLeuPheAeGluAsnGlu-----AlaLeuThrThrAlaIle	252
QY	878	ATGTCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAG-----	925
DB	253	GlyLysGlyGlyAlaValCysCysLeuProThrThrSerGlySerThrProValProIle	272
QY	926	GTCACCTCTCACTGGAATCAGATCTTACTCTTCAGCAACAATACATCCGACACAGCGGGA	985
DB	273	ValThrPheSerAspAsnLysGlnLeuValPheGluArgAsnHisSerIleMetGlyGly	292
QY	986	GGAGCTATCTATGTGAAAGAGTCGAATCGCTTCGCGAGGACTTACCTTATTCAGTAGA	1045
DB	293	GlyAlaIleTyrAlaAaGlyLysLeuSerIleSerSerGlyGlyProThrLeuPheIleAsn	312
QY	1046	AATAGTGTCAATGAGGTACAGCTCTCTTAAGGTGCGACCATGATCTCGAAGATAGTGG	1105
DB	313	AsnIleSerTyrAlaAsnSerGlnAsnLeuGlyGlyAlaIleAlaIleAspThrGlyGly	332
QY	1106	GAATTGAGTTTATCCGCGGATAGTGTGACATTTGCTTTTATAGGAATACAGTCACTTCT	1165
DB	333	GluIleSerLeuSerAlaGluLysGlyThrIleThrPheGlnGlyAsn-----ArgThr	350
QY	1166	ACTACTCTCGGACGAAATAGAGTAGTAGCTTAGCACTTAGGAACAGAGTCAAGATGACAGCT	1225
DB	351	SerLeuProPheLeuAsn-----GlyIleHisLeuLeuGlnAsnAlaLysPheLeuLys	368
QY	1226	TTGCGTTCTGCTGCTGATGAGCCATCTACTTCTATGATCCCATACTACAGGATCATCC	1285
DB	369	LeuGlnAlaArgAsnGlyTyrSerIleGluPheTyrAspProIleThr-----SerGlu	386
QY	1286	ACAACAGTTACAGATGCTTTAAAGATTAATGAGACTCCGCGAGATTTCTGCACACTACAAT	1345
DB	387	AlaAspGlySerThrGlnLeuAsnIleAsnGlyAspProLysAsnLys-----GluTyr	404
QY	1346	ACAGGGAACATCATCTTCACAGGAAAGATTTATCAGACACAGAGCCGCGAGATTTCTAAA	1405
DB	405	ThrGlyThrIleLeuPheSerGlyGluLys-----SerLeuAlaAsnAspProArg	421
QY	1406	AATCTTACTTCGAGGCTACTACAGCCTGTAACCTCTTTTCAGGAGTACTCTATCTTTAAAA	1465
DB	422	AspPheLysSerThrIleProGlnAsnValAsnLeuSerAlaGlyTyrLeuValIleLys	441
QY	1466	CATCGAGTGTACTCTGACAGCTCAGGATTCATCAACAGCAGGATTCCTGCTCGAAGATG	1525
DB	442	GluGlyAlaGluValThrValSerLysPheThrGlnSerProGlySerHisLeuValLeu	461
QY	1526	GACTGAGAACTACTCTTA---GAACCTGCTGATCTAGCACCATAAACAATTTGGTCAAT	1582
DB	462	AspLeuGlyThrLysLeuIleAlaSerLysGluAspIleAlaIleThrGlyLeuAlaIle	481
QY	1583	AACATCAGTTCTATPAGACGGTCAAGAGAGGCAAAA---ATAGAAACCAAGAGCTAGTCA	1639
DB	482	AspIleAspSerLeuSerSerSerSerThrAlaAlaValIleLysAlaAsnThrAlaAsn	501
QY	1640	AAAAATCTGATTTATCTGGAACCATCTTATTCGACCGGAGCGGCGGCTTTTATGAA	1699
DB	502	LysGlnIleSerValThrAspSerIleGluLeuIleSerProThrGlyAsnAlaTyrGlu	521
QY	1700	AATCATAGTTTAAAGAACTCTCAGTCTCAGCATCTTACAGCTCAAA-----GCTTCT	1753
DB	522	AspLeuArgMetArgAsnSerGlnThrPheProLeuLeuSerLeuGluProGlyAlaGly	541
QY	1754	GCACTGTAAACACACCGCA-----GTGACTCCAGATCTCTATATGGGT	1798
DB	542	GlySerValThrValThrAlaGlyAspPheLeuProValSerPro-----	556
QY	1799	GAGAAATTCATACGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGG---GGGACAGG	1855
DB	557	-----HisTyrGlyPheGlnGlyAsnTrp---LysLeuAlaTrpThrGlyThrGly	572
QY	1856	CTTCTAGACTGCAACCTTCACTGGACTAAACTGGCTATATTCCTATCCGAGCGT	1915
DB	573	---AsnLysValGlyGluPhePheTrpAspLysIleAsnTyrLysProArgProGluLys	591
QY	1916	ATCGGCTTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATAGCTCTCTCCAT	1975
DB	592	GluGlyAsnLeuValProAsnIleLeuTrpGlyAsnAlaValAspValArgSerLeuMet	611
QY	1976	TATCTTATGAGACTGCAACAGGAGGTTCCAGGAGACCGTCTCTTTTGGTGTCTGGA	2035
DB	612	GlnValGlnGluThrHisAlaSerSerLeuGluThrAspArgGlyLeuTrpIleAspGly	631
QY	2036	TTATCTACTCTTCTCCATAAGGATAGTACAAAAACACGACCGCGGTTTCGCCATTTGAGT	2095
DB	632	IleGlyAsnPhePheHisValSerAlaSerGluAspAsnIleArgTyrArgHisAsnSer	651
QY	2096	GGCGGTTATGTCATPAGAGGAAACCTACATACTTGTTCAGATAAGATTTCTTAGTGTGGA	2155
DB	652	GlyGlyTyrValLeuSerValAsnAsnGluIleThrProLysHisTyrThrSerMetAla	671

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QY 2156 TTTTGTACGCTCTTTGGAAGACATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTC 2215
Db 672 PheSerGlnLeuPheSerArgAspLysAspTyrAlaValSerAsnAsnGlnLysArgMet 691
QY 2216 TACGGAGGAACCTCTATTACACGACACAGAAACC-----TATATC 2257
Db 692 TyrLeuGlySerTyrLeuTyrGlnTyrThrThrSerLeuGlyAsnIlePheArgTyrAla 711
QY 2258 TCTCTTCTTGCAAACTACGGCCTTGTCTGTCTTATGTCTTATGTTCTTACAGAGATTCTCT--- 2314
Db 712 SerArgAsnProAsnValAsnValGlyIleLeuSerArgArgPheLeuGlnAsnProLeu 731
QY 2315 GTTCTCTTTTACGAAACCTTACTACCCATACGGAATACGATCTGAAACCAAGTAT 2374
Db 732 MetIlePheHisPheLeuCysAlaTyrGlyHisAlaThrAsnAspMetLysThrAspTyr 751
QY 2375 ACACATATCCTACTGTTAAGGAACCTGGGGAATGATAGTTTCTGCTTTAGATTCGGT 2434
Db 752 AlaAsnPheProMetValLysAsnSerTrpArgAsnAsnCysTrpAlaIleGluCysGly 771
QY 2435 GGAAGAGCTCCGATTGCTTAGATGAAGTGCT---CTATTGAGCAGTACATGCCCTTC 2491
Db 772 GlySerMetProLeuLeuValPheGluAsnGlyArgLeuPheGlnGlyAlaIleProPhe 791
QY 2492 ATGAAATTGCAGTTGTCTATGACATCAGAAAGGTTTAAAGAACACAGGGAACAGAGCT 2551
Db 792 MetLysLeuGlnLeuValTyrAlaTyrHisGlyAspPheLysGluThrThrAlaAspGly 811
QY 2552 CGTGAATTTGGAAGTACGCTCTGTGAATCTTGCTTACCTATCGGGATCCGATTGAT 2611
Db 812 ArgArgPheSerAsnGlySerLeuThrSerIleSerValProLeuGlyIleArgPheGlu 831
QY 2612 AAGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTGTTATCTACTGTGGATCTT 2671
Db 832 LysLeuAlaLeuSerGlnAspValLeuTyrAspPheSerPheSerTyrIleProAspIle 851
QY 2672 GTTCTGTAGTAACCCGACTGTACGACAACTACGGAATTAGCGGTGATCTTGGAAACC 2731
Db 852 PheArgLysAspProSerCysGluAlaLeuValIleSerGlyAspSerTrpLeuVal 871
QY 2732 TTGGTACGAATTTGGCAACAGCTTTAGCTTTCCTGTCGAGGAACCATTTTGGCTTT 2791
Db 872 ProAlaAlaHisValSerArgHisAlaPheValGlySerGlyThrGlyArgTyrHisPhe 891
QY 2792 AACTCAAATTTGAAGCCTTTAGCAATTTCTTTTGAATTCGCTGGGTCACTCTCGCAAT 2851
Db 892 AsnAspTyrThrGluLeuLeuCysArgGlySerIleGluCysArgProHisAlaArgAsn 911
QY 2852 TACAATGTAGCTTAGGAGCAAAATACCAATTC 2884
Db 912 TyrAsnIleAsnCysGlySerLysPheArgPhe 922

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RESULT 11
US-09-841-132-190
; Sequence 190, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yaser A.W.
; APPLICANT: Bhatia, Ajay
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-841-132-190

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Alignment Scores:
Pred. No.: 1006
Score: 1126.50
Percent Similarity: 46.02%
Best Local Similarity: 30.12%
Query Match: 20.83%
DB: 9
Gaps: 30

US-09-428-122-1 (1-3000) x US-09-841-132-190 (1-1006)

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Db 47 AspProSerGlyThrThrValPheSerAlaGlyGluLeuThrLeuLysAsnLeuAspAsn 66
QY 302 ACAGGCACAGCAATACAAAAGCTGTTTAAACAACACTAAGGGCGATTGTGCTTTCACA 361
Db 67 SerIleAlaLeuProLeuSerCysPheGlyAsnLeuLeuGlySerPheThrValLeu 86
QY 362 GGTAAACGGGAACCTCTATTGTTCCAAACGGTGGATGCAGGAGCTGTACAGGGGCTGCT 421
Db 87 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla 105
QY 422 GTTAAACAGCAGCGTGTAGATAAATCTACCACGTTTATAGGGTTTCTTCGCTATCTTT 481
Db 106 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe 125
QY 482 -----ATTGCGTCTCTGGAAGTTTCGATACTACCGGCAAGAGGCGGTT 526
Db 126 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 145
QY 527 AGCTGCTCTACGGGTAGC-----TTGAGT 550
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QY 551 TTGACAAAAAATCTCAGTTTTCGCTCTTCAGCAAAAACCTTTTCAACGATATATGCGGTGCT 610
Db 166 LeuLeuAsnAsnGlnLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyAla 185
QY 611 ATCACCGCAAAACTCTTTCATTAACAGGACTACAAATGTACAGCTCTGTTCTTCTGAAAT 670
Db 186 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn 205
QY 671 ACCTCTCTCAAGAAAGAGCGGAGCCATTACAGCTTCGATGCCCTTACCAATTACTTGGAAAC 730
Db 206 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValThrSerPheSerAlaMetAlaAsn 225
QY 731 CAAGGGGAAGTCTCTTT----- 748
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QY 749 -----TCTGACAATACTCTTCGGATTCT----- 772
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QY 773 -----GGAGCTGCAATT 784
Db 266 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaValGlyGlyIle 285
QY 785 TTTACAGAACGCTCGGTGACTATTCTTAATAATGCTAAAGTTTCTTTTATGCAAT--- 841
Db 286 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnVal 305
QY 842 -----AAGTCAACAGGAGCGGAGCTCTCTCAACACG 871
Db 306 AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 325
QY 872 GGGGATATG---TCAGGAGGTGCTATCTGTGCTTTATAA-----ACTAGT 913
Db 326 AsnAsnTyrGlyAspGlyGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 345
QY 914 ACAGATACTAAGGTACACCCCTACCTCGAAATCAGATGTTACTCTTTCAGCAACATACATCG 973
Db 346 AsnSerGlySerValSerPheAspGlyGluGlyValPhePheSerSerAsnValAla 365

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QY	974	ACAACAGCGGAGGAGCTATCTATGTGTAAGAAAGCTCGAACTGCGTTCGCGAGGACTTACC	1033
Db	366	AlaGlyLysGlyGlyAlaIleIyAlaLysLysLeuSerValAlaAsnCysGlyProVal	385
QY	1034	CTATTCTAGTAGAATAAGTGTCATGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATC	1093
Db	386	GlnPheLeuArgAsnIleAlaAsn-----AspGlyGlyAlaIleTyrLeu	400
QY	1094	GAAGATAGTGGGAAATGAGTTTATCCGCGAGTAGTGGTGCATGTCTCTTTTAGGGAAT	1153
Db	401	GlyGluSerGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn	420
QY	1154	-----ACAGTCACTTCTACTCTCTGGGACGAAT-----AGAAGT	1189
Db	421	LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln	440
QY	1190	AGTATCGACTTAGGAACGAGTGCAAAGATACACAGCTTTGGTTCCTCTCGTGTAGAGCC	1249
Db	441	AlaIleSerMetGlySerGlyGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln	460
QY	1250	ATCTACTTCTATGATCCCAATACTACAGGATCATCCACAACA-----GTTTACA	1297
Db	461	IleLeuPheAsnAspProIleGluMetAlaAsnGlyAlaAsnGlnProAlaGlnSerSer	480
QY	1298	GATGTCTTAAAGATTATGAGACTCCGGCAGATTTCTGCATACATAATATACAGGAACATC	1357
Db	481	LysLeuLeuLysIleAsnAspGlyGluGly-----TyrThrGlyAspIle	495
QY	1358	ATCTTCACAGGAGAAAGTTTATCAGACACAGAGCCGACAGATTTCTAAATCTTACCTCG	1417
Db	496	ValPheAla-----AsnGlySerSer	502
QY	1418	AAGCTACTACAGCCTGTAACTCTTTCAGGAGTACTCTATCTTTTAAACATGAGGATCAT	1477
Db	503	ThrLeuTyrGlnAsnValThrIleGluGlnGlyArgIleValLeuArgGluLysAlaLys	522
QY	1478	CTGCAGACTCAGGATTCACATCAACAGGAGATTCCTCGTTCGAATGGACGTAGGAATC	1537
Db	523	LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer	541
QY	1538	ACTCTAGAA-----CCTGCTGATACAGTAC-----	1561
Db	542	ThrLeuAspPheValThrProGlnProGlnProAlaAlaAsnGlnLeuIle	561
QY	1562	ACCATAACAATTTGGTCATTAAACATCAGTCTTATA-----	1597
Db	562	ThrLeuSerAsnLeuHisLeuSerLeuSerSerLeuLeuAlaAsnAsnAlaValThrAsn	581
QY	1598	-----GAGCGTGCAAAGAGCCAAATAATAGAAACCAAGCTACG	1636
Db	582	ProProThrAsnProProAlaGlnAspSerHisProAlaValIleGlySer---ThrThr	600
QY	1637	TCAAAATACTGACTTTATCTGGACCATCATCTTATTTGGACCCGCGGACGCTTTTAT	1696
Db	601	AlaGlySerValThrIleSerGlyProIlePhePheGluAspLeuAspAspThrAlaTyr	620
QY	1697	CAAAATCATACT--TTTAAAGAAATCCCTCAGTCCCTACGACATCTTTAGAGCTCAAGCTTCT	1753
Db	621	AspArgTyrAspTyrLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu---	639
QY	1754	GGAAGTGTAAACAGCAGCGAGTCACTCCAGATCTCTATATGGTGAGAATTC---CAT	1810
Db	640	GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys	659
QY	1811	TACGGCTATCAGGCAACTTGGGGCCCAATTTGTTGGGGCAGGGGCTTCTACAGCTGCA	1870
Db	660	TyrGlyTyrGlnGlySerTyrP---LysLeuAlaIleTyrAspProAsnThrAlaAsnAsnGly	678
QY	1871	ACCTTC-----AATGCACTAAACTGGCTATATCTCTAATCCGAGCGATTC	1918
Db	679	ProTyrThrLeuLysAlaThrTyrThrLysThrGlyTyrAsnProGlyProGluArgVal	698

Qy	1919	GGCTCTTTAGTCCTTAATAGCTTATGCAATGCATTTATAGATATATAGCTCTCTCCATTAT	1978
Db	699	AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer	718
Qy	1979	CTTATGGAGACTGCCAAACCAAGGGTTCGAGGGAGACCGTCTCTTTTGGTGTGCTGCATT	2038
Db	719	AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyLeuTrpValSerGlyVal	738
Qy	2039	TCTAACTCTTTCATGAAGATAGTACAAAACGACGCGGGTTTCGCCATTGTGAGTGC	2098
Db	739	SerAsnPhePheTyrHisaspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGly	758
Qy	2099	GGTTATGTCTAGGAGGAACCTTACATCTTGTTTCAGATAAGATTCTTAGTGTGCTGATT	2158
Db	759	GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer---SerMetPheGlyLeuAlaPhe	777
Qy	2159	TGTCAGCTCTTTCGAGAGATAGAGACTACTTGTGTAGCTTAAGAAATCAAGGTACAGTCTAC	2218
Db	778	ThrGluValPheGlyArgSerTyrAspTyrValValCysArgSerAsnHisAlaCys	797
Qy	2219	GGAGGAACCTCTTATACCAGCACACAAACCTATATCTCTCTCTGCAAACTACGG	2278
Db	798	IleGlySerValTyrLeuSerThrGlnGlnAlaLeu-----	809
Qy	2279	CCTTGTTCGTTGCTTATGTTCTCTACAGAGATCTCTGTTCTCTTTTCAGGA-----	2329
Db	810	---CysGly---SerTyr-----LeuPheGlyAspAlaPheIle	820
Qy	2330	AACCTTAGCTTACACCCATACGGATAACGATCTGAAACCAAGTATATACACATATCCTACT	2389
Db	821	ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysThrSerTyrThrPheAlaGluGlu	840
Qy	2390	GTTAAAGGAAGCTGGGGAAATGATGTTTCGCTTTAGAAATTCGGTGAAGAGCTCGATT	2449
Db	841	SerAspValArgTyrAspAsnAsnCysLeuAlaGlyGlnIleGlyAlaGlyLeuProIle	860
Qy	2450	TGCTTAGATGAAGTGCCTATTT---GAGCAGTACATGCCCTTCATGAATTCGACTTT	2506
Db	861	ValIleThrProSerLysLeuTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe	880
Qy	2507	GTCTATGCACATCAGGAAGGTTTAAAGACACGGGACACGAGCTCGTGAATTTGGAAGT	2566
Db	881	SerTyrAlaAspHisGluSerPheThrGluGluGlyAspGlnAlaargAlaPheLysSer	900
Qy	2567	AGCCGCTCTGTGAATCTTGCTTACCTATCCGATCCGATTCATTAAGGAATCAGACTGC	2626
Db	901	GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr	920
Qy	2627	CAAGATGCACAGTCAATCTACTCTTGGTTTATCTGTGATCTGTGCTAGTAGTACCCC	2686
Db	921	HisProAsnLysTyrSerPheMetalAlaTyrIleCysAspAlaTyrArgThrIleSer	940
Qy	2687	GACTGTACGACAACACTCGCAATTAGCGGTGATCTTGGAAAACTTCGGTACGAATTTG	2746
Db	941	GlyThrGluThrThrLeuLeuSerHisGlnGluThrTrpThrThrAspAlaPheHisLeu	960
Qy	2747	GCAAGACAAGCTTATGTCCTTCGTGACAGGAAACATTTTGTCTTAACTCAAAATTTTGA	2806
Db	961	AlaArgHisGlyValValValValArgGlySerMetTyrAlaSerLeuThrSerAsnIleGlu	980
Qy	2807	GCCTTTAGCCCAATTTCTTTTGAATTCGGTGGGTCTCTCGCAATTAACAATGAGACTTA	2866
Db	981	ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgGlyTyrGlyLeuSerAla	1000
Qy	2867	GGAGCAAAATACCAATTC	2884
Db	1001	GlySerLysValArgPhe	1006

RESULT 12
US-09-841-132-176
; Sequence 176, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:

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; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: fastseq for Windows Version 3.0/4.0
; SEQ ID NO 176
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Chlamydia
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(982)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-176

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Alignment Scores:

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Pred. No.:      9,89e-84      Length:      982
Score:          1124.50      Matches:      303
Percent Similarity: 45.92%      Conservative: 159
Best Local Similarity: 30.12%      Mismatches: 373
Query Match:      20.79%      Indels:      171
DB:              9          Gaps:      30

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US-09-428-122-1 (1-3000) x US-09-841-132-176 (1-982)

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QY 242 GAAGATGCTGGAACTACCTATTTAAGGGAATGTCTACTTAGAAAATATTCCTGGA 301
DB 23 AppProSerGlyThrValPheSerAlaGlyGluLeuThrLeuLysLeuAspAsn 42
QY 302 ACAGGCACGCAATCAAAAAAGCTGTTTAAACACATAAGCGGCAATTTGACTTTCACA 361
DB 43 SerIleAlaLeuProLeuSerCysPheGlyAsnLeuGlySerPheThrValLeu 62
QY 362 GCTAACGGAACTCTTATTTGCCAAACGGTGGATGACGAGGACTGTACAGGGCTGCT 421
DB 63 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla 81
QY 422 GTTAAACAGCAGCGTGAGTAAATCTACACGCTTTATAGGCTTTTCTCGTACTCTTT 481
DB 82 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe 101
QY 482 -----ATTGCTCTCTGGAAGTTTCGATTAACACCGGCAAGAGCGGCT 526
DB 102 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 121
QY 527 ACCTGCTCTACGGTAGC-----TTGAGT 550
DB 122 ThrProThrThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu 141
QY 551 TTGCAAAAATGTCAGTTTGCTCTTCAGCAAAACTTTTCAACGGATAATGCGCGTGCT 610
DB 142 LeuLeuAsnAsnGluLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyAla 161
QY 611 ATCAGCGCAAACTCTTTCAATTAACAGGACTACAAGTCAAGTCTGTTTCTGAAAT 670
DB 162 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn 181
QY 671 ACCTCTCAAGAAAGCGGCGCCATTTCAGACTTCGATTCGCTCCCTTACCATTACTGGAAC 730
DB 182 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValValThrSerPheSerAlaMetAlaAsn 201
QY 731 CAAGGGGAAGTCTCTTT----- 748
DB 202 GluAlaProIleAlaPheValAlaAsnValAlaGlyValArgGlyGlyIleAlaAla 221
QY 749 -----TGTGCAATACTTCTTCGATTCT----- 772
DB 222 ValGlnAspGlyGlnGlnGlyValSerSerThrSerThrSerThrGluAspProValValSer 241

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QY 773 -----GGAGCTCAATT 784
DB 242 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaArgValGlyGlyIle 261
QY 785 TTTACAGAAAGCCTCGTGACTATTCTAATATGCTAAAGTTTCTTTATTACCAAT--- 841
DB 262 TyrSerTyrGlyAsnValAlaPheLeuAsnGlyLysThrLeuPheLeuAsnVal 281
QY 842 -----AAGGTCACAGGAGCGAGTCTCTCAACAAG 871
DB 282 AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 301
QY 872 GGGGATATG---TCAGGAGGCTCTATCTGTGCTTATAA-----ACTAGT 913
DB 302 AsnAsnTyrGlyAspGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 321
QY 914 ACAGATACTAAGGTCACCTCCTCAGAAATCAGATGTTACTCTTCAGCAACAATACATCG 973
DB 322 AsnSerGlySerValSerPheAspGlyGluGlyValValPhePheSerSerAsnValAla 341
QY 974 ACAACAGCGGAGGAGCTATCTATGTGAAAGCTCGAACTCGACTGCTCCGAGGACTTACC 1033
DB 342 AlaGlyLysGlyAlaIleTyrAlaLysLysLeuSerValAlaAsnCysGlyProVal 361
QY 1034 CTATTTCAGTAGAATAGTGTCAATCGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATC 1093
DB 362 GlnPheLeuArgAsnIleAlaAsn-----AspGlyGlyAlaIleTyrLeu 376
QY 1094 GAAGATAGTGGGAATTCAGTTTATCCCGCATAGTGTGACATGTCTTTTAGGGAAT 1153
DB 377 GlyGluSerGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn 396
QY 1154 -----ACAGTCACCTTCTACTCTCTGGAGCAAT-----AGAAGT 1189
DB 397 LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln 416
QY 1190 AGTATCGACTAGGACGAGTGCAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCC 1249
DB 417 AlaIleSerMetGlySerGlyGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln 436
QY 1250 ATCTACTTCTATGATCCCACTAATACAGATCATCCACAACA-----GTTACA 1297
DB 437 IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnAsnGlnProAlaGlnSerSer 456
QY 1298 GATGCTTTAAAGTTAATGAGACTCCGCGACAGTTCGCACTACAATATACAGGGAACATC 1357
DB 457 LysLeuLeuLysIleAsnAspGlyGluGly-----TyrThrGlyAspIle 471
QY 1358 ATCTTCACAGGAGAAAGTTATCAGACAGAGCGCGCAGATTCTTAAAAATCTTACTTCG 1417
DB 472 ValPheAla-----AsnGlySerSer 478
QY 1418 AAGCTTACTACAGCCTGTAACTCTTTTCAGGAGTACTCTATCTTTTAAACATGGAGTGACT 1477
DB 479 ThrLeuTyrGlnAsnValThrIleGluGlnGlyArgIleValLeuArgGluLysAlaLys 498
QY 1478 CTGCAGACTAGGCAATTCACCTCAACAGCAGATTCGCTCTCGAAATCGAGCTAGGAAT 1537
DB 499 LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer 517
QY 1538 ACTCTAGAA-----CCTGCTGATCATAGC----- 1561
DB 518 ThrLeuAspPheValThrProGlnProGlnProProAlaAlaAsnGlnLeuIle 537
QY 1562 ACCATAACAATTTGGTCAATTAACATCAGTTCTATA----- 1597
DB 538 ThrLeuSerAsnLeuHisLeuSerLeuSerSerLeuLeuAlaAsnAsnAlaValThrAsn 557
QY 1598 -----GACGGTGCAGAGGCAAAAATAGAACCAACCTACG 1636
DB 558 ProProThrAsnProProAlaGlnAspSerHisProAlaValIleGlySer---ThrThr 576

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QY	743	TCTTTTCTGCAACTACTTCTTCGGATTCTCGAGCTGCAATTTTACAGAAGCCTCGGTG	802
Db	195	SerPheAlaArgAsnArgAlaAspLeuasnGlyGlyAlaileCysSerAsnLeuile	214
QY	803	ACTATTTCTAATAATGCTAAAGTTTCTTTATTGACAATAAGGTCACAGGAGCGAGCTCC	862
Db	215	CysSerGlyAsnValAsnProLeuPhePheThrGlyAsnSerAlaThr	230
QY	863	TCAACACGGGGATATGTCACGAGGTGCTATCTGTGCT	913
Db	231	-----AsnGlyGlyAlaileCysSilleSerAspLeuAsnThrSer	244
QY	914	ACAGATACTAAGGTCACCTCACCTGGGAATCAGATGTTACTTCTTCACGACAATACATCG	973
Db	245	GluIysGlySerLeuSerLeuAlaCysAsnGlnGluThrLeuPheAlaSerAsnSerAla	264
QY	974	ACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACCTGGCTTCGGAGGACTTACC	1033
Db	265	LysGluIysGlyGlyAlaileTyAlaIyshiMetValLeuArgTyAsnGlyProVal	284
QY	1034	CTATTCACTAGAAATAGTGTCOAATGGAGGTACAGCTCTTAAGGTGAGGCATAGCTATC	1093
Db	285	SerPheIleAsnAsnSer-----AlaIysilleGlyAlaileAlaile	299
QY	1094	GAAGATAGTGGGAATTGAGTTATCCGCCCATAGTGGTGACATGCTCTTTTAGGGAAT	1153
Db	300	GlnSerGlyGlySerLeuSerIleleuAlaGlyGluGlySerValLeuPheGlnAsnAsn	319
QY	1154	ACAGTCACTTCTACTACTCTCTGGGACGAATAGAATAGTAGTACACTTAGGAACGAGTGCA	1213
Db	320	SerGlnArgThrSerAspGlnGlyLeuValArgAsnAlaileTyLeu**LysAspAla	339
QY	1214	AAGATGACAGCTTTGCGTTCTGCTGCTGAGAGCACTACTTCTATGATCCCATAACT	1273
Db	340	IleLeuSerSerLeuGluAlaArgAsnGly---AspileLeuPhePheApproilleVal	358
QY	1274	ACAGGATCATCCACACAGTTTACAGATGCTCTTAAAAGTTAATGAGCTCCGGCAGATTCT	1333
Db	359	GlnGluSerSerSer-----lysGluSerProLeuProSer	370
QY	1334	GCATCAACAATACA-----	1348
Db	371	SerLeuGlnAlaSerValThrSerProThrProAlaThrAlaSerProLeuValIleGln	390
QY	1349	-----GGGAACATCATTTACAGGAGAAAAGTTATCAGACACAGAGCGCGCA	1396
Db	391	ThrSerAlaAsnArgSerSerValIlePheSerSerGluArgLeuSerGluGluLysThr	410
QY	1397	GATTCTAAAATCTTACTTCCAAGCTACTACAGCTCTTAATCTTTTCAGGAGGTACTCTA	1456
Db	411	ProAsp--AsnLeuThrSerGlnLeuGlnProIleGluLeuLysSerGlyArgLeu	429
QY	1457	TCTTTAAAACATGGAGTGACTCTCCAGACTCAGGCACTCACTCAACAGGCGAGATTTCGT	1516
Db	430	ValLeuIysAspArgAlaValLeuSerAlaProSerLeuSerGlnAspProGlnAlaLeu	449
QY	1517	CTCGAAATGGAGTAPGAACTACTCTAGAACCTCTGATACCTAGCACCAATAACAATTG	1576
Db	450	LeuIleMetGluAlaGlyThrSerLeuIlyshThrSerSerAspLeuIysLeuAlaThrLeu	469
QY	1577	GTCAATTAACTACGTCTTATAGACGGTCAAAGGCAAAATAGAAAACCAAGCTACG	1636
Db	470	SerIleProLeuHisSerLeuAspThrGluIysSerValThrIleHis-----	485
QY	1637	TCAAAAATCTGACTTTATCTGGAAACCATCACTTTATTGGACCGCAGCGCACTTTTAT	1696
Db	486	AlaProAsnLeuSerIleGlnLysIlePheLeuSerAsnSerGlyAspGluAsnPheTyR	505
QY	1697	GAATATCATAGTTTAAGAAATCTCTAGTCTCTACACACTCTTAGAGCTCAAGCTTCTGGA	1756
Db	506	GluAsnValGluLeuLeuSerLysGlnGlnAsnAnile---ProLeuLeuThrLeuPro	524

QY	1757	ACTGTAACAGCACCGCAGTGACTCTCCAGATTCCTATAATGGGTGAGAAATTCCTATTACGCC	1816
Db	525	LysGluInSerHisLeuHisLeuProAspGlyAsnLeuSer-----HisPheGly	542
QY	1817	TATCAGGGAACTTGGGGCCCCAATTTGTTGG-----GGGACAGGGGCTTCTACCACT	1867
Db	543	TyrGlnGlyAspTrp---ThrPheSerTrpIlysAspSerAspGluGlyHisSerLeuIle	561
QY	1868	GCAACCTTCAACTGGCATATAAACCTGGCTATATCTTAATCCGAGCGCTATCGGCTCTTTA	1927
Db	562	Ala-----AsnTrpThrProLysAsnTyrValProHisProGluArgGlnSerThrLeu	579
QY	1928	GTCCCTAATAGCTTATCGAATGCATTATAGATTAATTAGCTCTCTCCATTATCTATTAGGAG	1987
Db	580	ValAlaAsnThrLeuTrpAsnThrTyrSerAspMetGlnAlaValGlnSerMetIleAsn	599
QY	1988	ACTGCAACAAGAGGTTGCGAGGAGACCGTGCTTTT-----TCGTGTGCTGATATCT	2041
Db	600	ThrThrAlaHisGly-----GlyAlaTyrLeuPheGlyThrTrpGlySerAlaValSer	617
QY	2042	AACCTCTTTC-----CATAGAAGTAGTACAAAAACACGACGCGGTTTCCCACTTTGAGT	2095
Db	618	AsnLeuPheTyrValHisAspSerSerGlyLysProIleAspAsnTrpHisHisArgSer	637
QY	2096	GGCGGTTATGTCATAGGAGGAACCTACATACCTTGTTCAGATAAGATTCCTAGTGTGCA	2155
Db	638	LeuGlyTyrLeuPheGlyIleSerThrHisSerLeuAspHisSerPheCysLeuAla	657
QY	2156	TTTTGTTCAGCTCTTTGGAAGAGATAGAGACTACTTTTGTAGCTAAGAAATCAAGTCAAGTC	2215
Db	658	AlaGlyGlnLeuLeuGlyLysSerAspSerPheIleThrSerThrGluThrThrSer	677
QY	2216	TACGGAGGAACCTCTCTATTACCAGCACCAACCAACCTATATCTCTCTCTTCGCAAACTA	2275
Db	678	TyrIleAlaThrValGlnAlaGlnLeuAlaThrSerLeuMethIysIle-----	693
QY	2276	CGGCCTTGTTGTTGCTTATGTTCTCCACAGAGATTCCTGTTCTCTTTTCAGGAAACCTT	2335
Db	694	-----SerAlaGlnAla	697
QY	2336	AGCTACACCATACGGTAACGATCTGAAACCAAGTATACACATATCCTACTGTAAA	2395
Db	698	CystyrAsnGluSerIleHisGluLeuLysThrLysTyrArgSerPheSerLysGluGly	717
QY	2396	---GGAAGCTGGGGGAATAGTATTCCGTTTGAAGATTCGGTGGAGAGCTCCGATTTGC	2452
Db	718	PheGlySerTrpHisSerValAlaValSerGlyGluValCysAlaSerIleProIleVal	737
QY	2453	TTAGATGAAGTGCTCTATTGTAGCAGTACATCCCTTCATGAAATTCGAGTTTGTCTAT	2512
Db	738	SerAsnGlySerGlyLeuPheSerSerPheSerIlePheSerLysLeuGlnGlyPheSer	757
QY	2513	GCACATCAGAAAGGTTTAAAGAACAGGGAACAGAGAGCTCGTGAAATTGGAAGTAGCCGT	2572
Db	758	GlyThrGlnAspGlyPheGluGluSerSerGlyGluIleArgSerPheSerAlaSerSer	777
QY	2573	CTTGTGAATCTTGCTTACCTATCTCGGATCCGATTTGATAAGGAATCAGACTCCCAAGAT	2632
Db	778	PheArgAsnIleSerLeuProIleGlyIleThrPheGluLysLysSerGln---LysThr	796
QY	2633	GCAACGPACAAATCTAATCTTGGT---TAPACTGTGGATCTCTGCTAGTACACCCGAC	2689
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QY	2690	TGTACGCAACACTCGGAATTACGGGTGATTTCTTGGAAACCTTCGGTACGAATTTGGCA	2749
Db	817	GlyProValValLeuLeuLysAsnAlaValSerTrpAspAlaProMetAlaAsnLeuAsp	836
QY	2750	AGACAAGCTTAGTCTCTGTCGAGGGAACCATTTTGTCTTAACTCAAATTTTGAAGCC	2809
Db	837	SerArgAlaTyrMetPheArgLeuThrAsnGlnArgAlaLeuHis---ArgLeuGlnThr	855
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Db      856 LeuLeuAsnValSerCysValLeuArgGlyGlnSerHisSerThrLeuAspLeuGly 875
      2870 GCAAAATACCAATTC 2884
      876 ThrThrTyrArgPhe 880

RESULT 14
US-09-841-132-189
; Sequence 189, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yaser A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 189
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Chlamydia
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(866)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-189

Alignment Scores:
Pred. No.: 1,2e-61 Length: 866
Score: 856.00 Matches: 260
Percent Similarity: 44.28% Conservative: 123
Best Local Similarity: 30.06% Mismatches: 368
Query Match: 15.83% Indels: 114
DB: 9 Gaps: 24

US-09-428-122-1 (1-3000) x US-09-841-132-189 (1-866)
Qy      452 ACGTTTATAGGTTTCTTCGCTATCTTTATTCGGCTCTCGAAGTCGATTAACATACC 511
Db      452 SerTyrCysTrpPheValSerLysLeuHisIleThrAspProLysGluAlaLeuPheLys 81
      512 GGCAAGGAGCGGTAGC-----TGCTCTACG 538
      82 GluLysGlyAspLeuSerIleGlnAsnPheArgPheLeuSerPheThrAspCysSerSer 101
      539 -----GGTAGCTTGAGTTTGACAAAAAT 562
      102 LysGluSerSerProSerIleIleHisGlnLysAsnGlyGlnLeuSerLeuArgAsnAsn 121
      563 GTCAGTTTGCTTCAGCAAAACTTTTCAAGGATATGCGGTCGTATCAGCGCAAAA 622
      122 GlySerMetSerPheCysArgAsnHisAlaGluGlySerGlyGlyAlaIleSerAlaAsp 141
      623 ACTCTTTCATTACAGGAGCTACAAATGTCAGCTCTGTTTCTGAAATACCTCTCAAG 682
      142 AlaPheSerLeuGlnHisAsnTyrLeuPheThrAlaPheGluGluAsnSerSerLysGly 161
      683 AAAGCGGAGCCATTACAGATCCGATCCCTTACCATTTACTGAAACCAAGGGGAAGTC 742
      162 AsnGlyGlyAlaIleGln--AlaGlnThrPheSerLeuSerArgAsnValSerProIle 180
      743 TCTTTTCTGCAATACTTCTTCGGAATCTCGAGCTGCAATTTTACAGAGCCCTCGGTG 802
      181 SerPheAlaArgAsnArgAlaAspLeuAsnGlyGlyAlaIleCysCysSerAsnLeuIle 200
      803 ACTATTCTTAATAGCTAAAGTTTCCTTTATTGACATAAGGTCACAGGAGCGAGCTCC 862
      201 CysSerGlyAsnValAsnProLeuPhePheThrGlyAsnSerAlaThr----- 216

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Qy      863 TCAACAACGGGGATATGTCACGAGGTGCTATCTGTGCT-----TATAAAACTAGT 913
      217 -----AsnGlyGly***IleCysCysIleSerAspLeuAsnThrSer 230
      914 ACAGATACTAAGGTCACCTCCTCAGTGAATCAGATGTTACTCTTCAGCAACAATACG 973
      231 GluLysGlySerLeuSerLeuAlaCysAsnGln***ThrLeuPheAlaSerAsnSerAla 250
      974 ACAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTCGAGTCTCCGGAGGACTTACC 1033
      251 LysGluLysGlyGlyAlaIleTyrAlaLysHisMetValLeuArgTyrAsnGlyProVal 270
      1034 CTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGTGGAGCATAGTATC 1093
      271 SerPheIleAsnAsnSer-----AlaLysIleGlyGlyAlaIleAlaIle 285
      1094 GAAGATAGTGGGGAATTGAGTTTATCCGCGATAGTGGTACATGTTGTTTGTAGGGAAT 1153
      286 GlnSerGlyGlySerLeuSerIleLeuAlaGlyGluGlySerValLeuPheGlnAsnAsn 305
      1154 ACAGTCACTTCTACTCTCTCGGAGCAATAGAAAGTAGTAGTACGACTTAGAACGAGTGCA 1213
      306 SerGlnArgThrSerAspGlnGlyLeuValArgAsnAlaIleTyrLeuGluLysAspAla 325
      1214 AAGATGACAGCTTTGCGTCTGCTGTGTAGAGCATCTACTTCTATGATCCCATAACT 1273
      326 IleLeuSerSerLeuGluAlaArgAsnGly--AspIleLeuPhePheAspProIleVal 344
      1274 ACAGGATCATCCACACAGTACAGATGTTTAAAGTTAATGAGACTCGGCGAGATTCT 1333
      345 GlnGluSerSerSer-----LysGluSerProLeuProSer 356
      1334 GCACATCAATATACA----- 1348
      357 SerLeuGlnAlaSerValThrSerProThrProAlaThrAlaSerProLeuValIleGln 376
      1349 -----GGGAACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGCGCGCA 1396
      377 ThrSerAlaAsnArgSerValIlePheSerSerGluArgLeuSerGluGluLysThr 396
      1397 GATCTTAAATCTTACTTCGAGCTACTACACCTGTAACTCTTTTCAGAGGACTACTCTA 1456
      397 ProAsp--AsnLeuThrSerGlnLeuGlnGlnProIleGlnLeuLysSerGlyArgLeu 415
      1457 TCTTTTAAACATCGAGTGACTCTCGACTCAGCATTCCTCAACAGGAGGAGTCTCTCGT 1516
      416 ValLeuLysAspArgAlaValLeuSer***ProSerLeuSerGlnAspProGlnAlaLeu 435
      1517 CTCGAATGACGTAGGAACCTACTCTAGAACCTGCTGATAGTACCATTAACAATTG 1576
      436 LeuIleMetGluAlaGlyThrSerLeuLysThrSer***AspLeuLysLeu***Thr*** 455
      1577 GTCATTAAACATCAGTCTATAGACGGTGCAGAGGCAAGGCAAAATAGAACCAAGCTACG 1636
      456 SerIleProLeuHisSerLeuAspThrGluLysSerValThrIleHis----- 471
      1637 TCAAAAATCTGACTTTTATCTGGAACCATCATCTTATTGGACCCGAGCGGACGTTTAT 1696
      472 AlaProAsnLeuSerIleGlnLysIlePheLeuSerAsnSerGlyAspGluAsnPheTyr 491
      1697 GAAATCATAGTTTAGAAATCTCTAGCTCTAGCTCTAGCTCTAGCTCTAGCTCTAGCTCTGGA 1756
      492 GluAsnValGluLeuSerLysGluGlnAsnAsnIle---ProLeuLeuThrLeuPro 510
      1757 ACTGTAACAGACCCGAGTCACTCCAGATCTTATATGGGTGAGAAATCCATTACGGC 1816
      511 LysGluGlnSerHisLeuHisLeuProAspGlyAsnLeuSerSer-----HisPheGly 528
      1817 TATCAGGGAACCTTGGGGCCCAATTGTTTGG-----GGGACAGGCGCTTCTACGACT 1867
      529 TyrGlnGlyAspTrp---ThrPheSerTrpLysAspSerAspGluGlyHisSerLeuIle 547

```



```
Db 143 ----- 143
QY 755 AATACITCTTCGGATTCGGAGTCGCAATTTTACAGAAGCCCTCGGTGACTATTCTTAAT 814
Db 144 -----ValleTySerAsnSerValLeuLeuGluAsn 155
QY 815 AATGCTAAAGTTTCCTTTATTGCAATAGTTCACAGGAGGAGCTCCTCAACAACGGGG 874
Db 156 AsnSerGlnGlySerSerGlyLeuAsnLysSerAlaGly ----- 168
QY 875 GATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACCTAAGTCAACC- 931
Db 169 -----LysGlyValPheLeuCysGlyLys---SerThrAspValGlyAlaThrSer 185
QY 932 -----CTCAGTGAATACAGATGTTACTCTTCAGCAACAATACATCGACAACA 979
Db 186 ProThrLeuLeuLeuArgAsnAsnGlyGluPheLeuThrValGlyAsnAlaAlaThrSer 205
QY 980 CGGGAGGAGCTATCTATGTGAAGAAGCTCGAAGTGGCTCCGAGGAGCTACCTATTC 1039
Db 206 SerGlyAlaAlaIleTyAlaGluLysMetIleLeuSerSerGlyGlyTyThrLysPhe 225
QY 1040 AGTAGAATAGTGTCAATGGAGGTACAGCTCCTAAAGTGGAGCATAGCTATCGAAGAT 1099
Db 226 GlnSerAsnVal-----SerTyAspGlnGlyAlaIleAlaAlaPro 241
QY 1100 AGTGGGAATGAGTTTATCGCGCATAGTGTGACATGTGCTTTTGGGAATACAGTC 1159
Db 242 AsnGlyGluLeuSerLeuSerAlaAspLysGlyAsnIleValPheGluArgAsnLeuLys 261
QY 1160 ACTTCTACTCTCTGGAGCAATAGAAAGTAGTAGTACGACTAGGAACGAGTGAAGATG 1219
Db 262 IleAlaAsnLysGlnAsnThr---ProAsnAlaIleHisLeuGlyAspAsnAlaLysPhe 280
QY 1220 ACAGCTTTGGTGTGCTGTGTGAGAGCCATCTACTTCTATGATCCATAACTACAGGA 1279
Db 281 LeuGlnLeuArgAlaAlaAsnAsnLysAlaIlePheTyAspProIleThrThr 300
QY 1280 TCATCCACACAGTTACAGATGCTTAAAGTTAATGAGACTCGCGGAGATTCGCACTA 1339
Db 301 GlySer-----ValAlaAspArgLeuIleIleAsnAsnSerGlnGlyGlu--AlaSer 317
QY 1340 CAATATACAGGACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGCGCCAGAT 1399
Db 318 ThrTyAspGlyAlaIleValPheSerSerLeuAsnLeuPhe---ThrHisSerProGlu 336
QY 1400 TCTAAAAATCTTACTTCCAGACTACTACAGCTCTAACTCTTTCAGGAGGTACTCTATCT 1459
Db 337 CysLys-----LeuSerSerPheSerGlnGlyLeuThrLeuAlaAlaGlySerLeuVal 354
QY 1460 TTAACAATGAGTGCATCTGCAGACTCAGGCATCTACACAGGAGATTCCTGCTCTC 1519
Db 355 LeuGluGluGlyValCysValGlnAlaProSerPheAspGlnArgAlaHisSerGlnLeu 374
QY 1520 GAAATGGAGCTGAGGAATCTACTCTAGAACCTGCTGATAGCACCAATAACAATTTGGTC 1579
Db 375 PheMetAsnProGlyThrLysLeuGlnAlaThrGlnAsnIleSerValLysAsnLeuHis 394
QY 1580 ATTAACATCAGTTCTATAGAGCGGTGCAAGAAGGCAAAAATAGAAAACCAAGCTACGTC 1639
Db 395 LeuAsnLeuAsnArgIle---AlaGluGluProAlaTyIleThrThrAspAspAla 413
QY 1640 AAAAATCTGATTTATCGGAACCATCATCTTATTGGACCGCAGCGGCACGTTTATGAA 1699
Db 414 SerSerValAspIleCysGlyProValValMetHisIleAspAspGluIlePheTyAsn 433
QY 1700 AATCATAGTTTAAGAAATCCTCAGTCTCAGCATCTTAGAGCTCAAGCTTCT- 1753
Db 434 GlnThrValLeuAlaAsnGluLeuSerValGluCysLeuAsnLeuSerProHisLeu 453
QY 1754 GGAACCTGTACAGCAGCGCAGTCTCAGATCCAGATCCTATATGGGTGAGAAATCCATTAC 1813
Db 1813 ----- 1813
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Db 454 AspAsnIleThrIleAspAspValProAlaValProIleMetThrLeuGluSerHisArg 473
QY 1814 GGCTATCAGGGAACCTTTGGGCCCCAATTTGTTGGGGACA-----GGG 1855
Db 474 GlyTyArgGlnGlyThrTrp---GluIleSerTrpLysGluGlnProLysLeuThrPheGly 492
QY 1856 GCTTCTACGACTGCAACC-----TTCAACTGGACTAAAACCTGGCTATATT 1900
Db 493 LysAlaThrIleAlaProAsnLysGlnMetHisLeuIleTrpLysProSerGlyTyVal 512
QY 1901 CCT-----AATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATCGAAT 1948
Db 513 ProPheSerGlyGlyThrGlyGluPheThrThrSerLeuValProAsnSerLeuTrpAsn 532
QY 1949 GCATTTATGATATTAGTCTCTCCATTATCTTATGAGACTGCAACCAAGGTTTCAG 2008
Db 533 LeuPheLeuAspThrArgPheSerGlnGlnAlaIleGlu-----LysHisAlaValSer 550
QY 2009 GGAGACCGTGCTTTTGGTGTCTGCGATTATCTAACTTCTTCCATAAGGATAGTACAAA 2068
Db 551 SerGlyAsnGlyIleTrpIleSerMetThrAsnSerPheLeuGlnGlySerThrAsn 570
QY 2069 ACACGACGGGGTTTCGCCATTTGAGTGGCGGTATGTCTATAGAGGAAAACCTACATACT 2128
Db 571 AsnAsnHisGlyPheArgHisLysSerSerGlyTyThrAlaGlyGlyLysIleGlnThr 590
QY 2129 TGTTTCAGATAAGATTCTTGTAGTGTGCTGCTGCTTTGTGCTCTTTTGGAAAGATAGACTAC 2188
Db 591 LeuGlnAspAspIlePheSerValSerPheSerGlnLeuPheGlyArgSerLysAspPhe 610
QY 2189 TTTGTAGCTAAGAAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCGACCAACGAA 2248
Db 611 GlySerAlaThrSerLysAspThrPheLeuSerGlySerIleTyThrAlaGlnHisSerArg 630
QY 2249 -----ACCTATATCTCTCTCTCTTCTTCTTCAAACTACGGCTTCTGCTGTG 2290
Db 631 ArgLeuLeuProIleMetArgPheLeuAlaGlyThrSerThrTyArgProArgLeuLeu 650
QY 2291 TCTTATGTTCTACAGAGATTCTGTTCTCTTTTTCAGGAAACCTTACGACCCATACG 2350
Db 651 LeuSerIleProLysAsnLeuProIleAsnPheAspValLeuValSerTySerTyAsp 670
QY 2351 GATAACGATCTGAAAACCAAG 2371
Db 671 SerAsnHisMetLysValGln 677
```

Search completed: December 16, 2003, 10:53:00
Job time : 178.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 16, 2003, 10:21:34 ; Search time 48.5 seconds

(without alignments)
11897.157 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 5409

Sequence: 1 cgcctctacacgtagaggt.....tgctttgctaaacacatttc 3000

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US09428122/runat_16122003_102128_10789/app_query.fasta_1.3143
-DB=PIR_76 -QFMT=fastan -SUFFIX=trp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=oct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09428122@cgn_1_1_75 @runat_16122003_102128_10789 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_76.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3991	73.8	772	2	H86492
2	2058	38.0	928	2	G86546
3	2058	38.0	928	2	G81591
4	1982	36.6	928	2	E86546
5	1982	36.6	928	2	E72077
6	1965	36.3	936	2	C72078
7	1964	36.3	936	2	C86546
8	1964	36.3	936	2	B81591
9	1940	35.9	930	2	D86546
10	1940	35.9	930	2	A81591
11	1936	35.8	930	2	D72078
12	1868	34.5	949	2	F81591
13	1855	34.3	928	2	H86546
14	1855	34.3	928	2	D72077

15	1580.5	29.2	841	2	E72130	polymorphic membra
16	1444	26.7	1276	2	B86546	polymorphic outer
17	1444	26.7	1276	2	C81591	polymorphic membra
18	1442.5	26.7	922	2	B72131	polymorphic outer
19	1442.5	26.7	922	2	E86491	polymorphic outer
20	1441.5	26.7	922	2	F81539	polymorphic membra
21	1384.5	25.6	995	2	C81593	polymorphic membra
22	1383.5	25.6	1407	2	B72078	polymorphic outer
23	1377.5	25.5	973	2	B86547	polymorphic outer
24	1377.5	25.5	973	2	F72076	polymorphic outer
25	1253.5	23.2	712	2	E86492	polymorphic outer
26	1120.5	20.7	1013	2	G71460	probable outer mem
27	1051	19.4	987	2	H81722	polymorphic outer
28	1017.5	18.8	445	2	E86493	polymorphic membra
29	917	17.0	186	2	G86492	polymorphic outer
30	916	16.9	359	2	C86493	polymorphic outer
31	911	16.8	867	2	F81721	polymorphic membra
32	863	16.0	878	2	B71460	probable outer mem
33	821	15.2	494	2	D86493	polymorphic outer
34	792	14.6	427	2	A86493	polymorphic outer
35	685.5	12.7	1609	2	A86611	polymorphic membra
36	685.5	12.7	1609	2	G72013	polymorphic outer
37	672.5	12.4	978	2	H72076	polymorphic outer
38	670	12.4	947	2	G86557	polymorphic membra
39	667.5	12.3	978	2	B81593	polymorphic outer
40	667.5	12.3	978	2	C86547	polymorphic membra
41	666	12.3	947	2	D72067	polymorphic outer
42	666	12.3	1723	2	H86557	polymorphic membra
43	666	12.3	1723	2	E72067	polymorphic membra
44	666	12.3	1732	2	C81601	polymorphic membra
45	665.5	12.3	946	2	C86549	polymorphic outer

ALIGNMENTS

RESULT 1

H86492

Pmp_3 [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001

R:Accession: H86492

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Ouchi, K.; Shiba, T.;

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: H86492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-772 <STO>

A:Cross-references: GB:BA000008; NID:G8978389; PIDN:BAA98226.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: pmp_3_2

Alignment Scores:

Pred. No.:	8.16e-245	Length:	772
Score:	3991.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.87%	Mismatches:	0
Query Match:	73.78%	Indels:	0
DB:	2	Gaps:	0

US-09-428-122-1 (1-3000) x H86492 (1-772)

QY	569	TTGCTCTTCAGCAAAACCTTTTCAACGGATAATGCGGTGCTATCACCGCAAAACCTCTT	628
Db	1	MetLeuPheSerLysAsnPheSerThrAspAsnGlyGlyAlaIleThrAlaLysThrIeu	20
QY	629	TCATTAAACAGGAGCTACAAATCTGCTCTGTTTCTGAAAAATACCTCTCAAGAAAGGC	688
Db	21	SerLeuThrGlyThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLysLysGly	40
QY	689	GGAGCCATTGAGACTTCGGATCCCTTACCATTACTGGAAACCAAGGGAGGACTCTCTTTT	748

Db 41 GlyAlaIleGlnThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyLeuValSerPhe 60
QY 749 TCTGACAAATCTCTTCCGATTCGAGCTGCAATTTTACAGAAAGCCTCGGTGACTATT 808
Db 61 SerAspAsnThrSerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIle 80
QY 809 TCTAATAATGCTAAAGTTCTCTTATTGACAAATAGGTCACAGAGCGAGCTCTCAACA 868
Db 81 SerAsnAsnAlaLysValSerPheIleAspAsnLysValThrGlyAlaSerSerThr 100
QY 869 ACGGGGATATGTCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACCTAAGGTC 928
Db 101 ThrGlyAspMetSerGlyGlyAlaIleCysAlaIleThrSerThrAspThrLysVal 120
QY 929 ACCCTCACTGGAATCAGATTGTTACTCTTCAGCAACAATCATCGACAAAGCGGGAGGA 988
Db 121 ThrLeuThrGlyAsnGlnMetLeuLeuPheSerAsnAsnThrSerThrAlaGlyGly 140
QY 989 GCTATCTATGTGAAAAAGCTCGAACTCGCTTCGGAGGACTTACCTATTTCAGTAGAAAT 1048
Db 141 AlaIleThrValLysLysLeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerArgAsn 160
QY 1049 AGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAA 1108
Db 161 SerValAsnGlyGlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGlu 180
QY 1109 TTGAGTTTATCCCGCATGATGTTGACATTGTCTTTTATGGGAATACAGTCATCTACT 1168
Db 181 LeuSerLeuSerAlaAspSerGlyAspIleValPheLeuGlyAsnThrValThrSerThr 200
QY 1169 ACTCTCGGACGAAATAGAACTAGTATCGACTTAGGACGAGTCAAGAGATGACAGCTTTC 1228
Db 201 ThrProGlyThrAsnArgSerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeu 220
QY 1229 CGTCTGCTCTGGTAGAGCATCTACTTCTATGATCCCACTACAGAGTATCCACA 1288
Db 221 ArgSerAlaAlaGlyArgAlaIleThrPheThrAspProIleThrThrGlySerSerThr 240
QY 1289 ACAGTTACAGATGCTTAAAGTTAATGACATCCGCGAGATCTGACATCAATATACA 1348
Db 241 ThrValThrAspValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnThr 260
QY 1349 GCGAACATCATCTTCAGGAGAAAGTTATACAGACAGACGCGCAGATTTCTAAAT 1408
Db 261 GlyAsnIleIlePheThrGlyGlyLysLeuSerGluThrGluAlaAlaAspSerLysAsn 280
QY 1409 CTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGAGGTACTCTATCTTTAAACAT 1468
Db 281 LeuThrSerLysLeuLeuGlnProValThrLeuSerGlyGlyThrLeuSerLeuLysHis 300
QY 1469 GGAGTGACTCTGAGACTCGGATTCACCTCAACAGCAGATCTCGTCTCGAAATGGAC 1528
Db 301 GlyValThrLeuGlnThrGlnAlaPheThrGlnGlnAlaAspSerArgLeuGluMetAsp 320
QY 1529 GTAGGAAGTACTCTAGAACCTGTGTACTAGACACATAAACAATTTGGTCATTAAACATC 1588
Db 321 ValGlyThrThrLeuGluProAlaAspThrSerThrIleAsnAsnLeuValIleAsnIle 340
QY 1589 AGTTCTATAGACGGTGCAGAGAGGCAAAATAGAAACCAAGCTACGTCAGAAATCTGT 1648
Db 341 SerSerIleAspGlyAlaLysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeu 360
QY 1649 ACTTTATCGAACCATCACTTTATGACCCGACCGGACGTTTATGAAATCATAGT 1708
Db 361 ThrLeuSerGlyThrIleThrLeuLeuAspProThrGlyThrPheThrGluAsnHisSer 380
QY 1709 TTAAGAAATCCTCAGTCTACGACATCTTAGAGCTCAAGCTCTCGAAGCTGAAACAGC 1768
Db 381 LeuArgAsnProGlnSerThrAspIleLeuGluLeuLysAlaSerGlyThrValThrSer 400
QY 1769 ACCGAGTACTCCAGATCTCTAATGGGTGAGAAATTCATTTACGGCTATCAGGAACT 1828

Db 401 ThrAlaValThrProAspProIleMetGlyGlyLysPheHisThrGlyThrGlnGlyThr 420
QY 1829 TGGGGCCCAATTTGTTGGGGACAGGGGCTTTACAGCTGCAACCTTCAACTGGACTAAA 1888
Db 421 TrpGlyProIleValTrpGlyThrGlyAlaSerThrThrAlaThrPheAsnTrpThrLys 440
QY 1889 ACTGGCTATATTCCTAATCCCGAGCGCTATCGGCTCTTTAGTCCCTAATAGTCTATGGAAT 1948
Db 441 ThrGlyThrIleProAsnProGluArgIleGlySerLeuValProAsnSerLeuTrpAsn 460
QY 1949 GCATTTATAGATTAAGTCTCTCCATTAATCTTATGAGAGCTGCAAAAGAGGTGGCAG 2008
Db 461 AlaPheIleAspIleSerSerLeuHisThrLeuMetGluThrAlaAsnGluGlyLeuGln 480
QY 2009 GGAGACGGTGTCTTTTGGTGTGCTGGAATTAATCTTCTCCATAAGGATAGTACAAA 2068
Db 481 GlyAspArgAlaPheTrpCysAlaGlyLeuSerAsnPheHisLysAspSerThrLys 500
QY 2069 ACACGACGGGTTTCGCCATTTGAGTGGGGTGTATGTCATAGGAGGAAACCTACATACT 2128
Db 501 ThrArgArgGlyPheArgHisLeuSerGlyGlyThrValIleGlyAsnLeuHisThr 520
QY 2129 TGTTCAGATAAGATTTCTAGTGTCTGATTTTGCAGCTCTTTGGAAGAGATAGACTAC 2188
Db 521 CysSerAspLysIleLeuSerAlaAlaPheCysGlnLeuPheGlyArgAspArgAspThr 540
QY 2189 TTTGTAGTAAAGATCAAGTACAGTCTACGGAGGAACCTCTTATTTACCAGCACACGAA 2248
Db 541 PheValAlaLysAsnGlnGlyThrValThrGlyGlyThrLeuThrThrGlnHisAsnGlu 560
QY 2249 ACCTATATCTCTCTTCCCTTGCACACTACGGCCTTGTCTGTTGTTATGTTCTCTACAGAG 2308
Db 561 ThrThrIleSerLeuProCysLysLeuArgProCysSerLeuSerThrValProThrGlu 580
QY 2309 ATTCTGTCTCTCTTTTCAGGAAACCTTAGCTACACCATACGGATAACCATCTGAAAAC 2368
Db 581 IleProValLeuPheSerGlyAsnLeuSerThrHisThrAspAsnAspLeuLysThr 600
QY 2369 AGTATACAACTATCTCTACTGTAAAGAGCTGGGGAATGATAGTTTCGCTTTAGAA 2428
Db 601 LysThrThrThrThrProThrValLysGlySerThrGlyAsnAspSerPheAlaLeuGlu 620
QY 2429 TTCGGTGAAGAGCTCCGATTTCTTAGTAGAAGTCTTATTCAGCAGTACATGCCCC 2488
Db 621 PheGlyGlyArgAlaProIleCysLeuAspGluSerAlaLeuPheGluGlnThrMetPro 640
QY 2489 TTCATGAAATTCAGTCTTGTCTATGCACATCAGGAGGTTTAAAGAACAGGAAACAGAA 2548
Db 641 PheMetLysLeuGlnPheValThrAlaHisGlnGluGlyPheLysGluGlnGlyThrGlu 560
QY 2549 GCTCGTGAATTTGGAAGTAGCCGTCTTGTGAATCTTTCCTTACCTATCGGATCCGATTT 2608
Db 661 AlaArgGluPheGlySerSerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPhe 680
QY 2609 GATAAGGAATCAGACTGCCAAGATGCAAGTACATCTAATCTTGGTTATATCTGGAT 2668
Db 681 AspLysGluSerAspCysGlnAspAlaThrThrAsnLeuThrLeuGlyThrValAsp 700
QY 2669 CTTGTTCTGTPAGTAACCCGACTGTACGACCACTCGCAATTAGCGGTGATTTCTGGAAA 2728
Db 701 LeuValArgSerAsnProAspCysThrThrThrLeuArgIleSerGlyAspSerThrLys 720
QY 2729 ACCTTCGGTACCAATTTGGCAAGACAGCTTTAGTCTTCTTCGTCGAGGGAACCATTTTGC 2788
Db 721 ThrPheGlyThrAsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCys 740
QY 2789 TTTAACCTAAATTTGAAGCTTTAGCCAAATTTCTTTGAAATTCGCTGGTCACTCGC 2848
Db 741 PheAsnSerAsnPheGluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArg 760
QY 2849 AATTACAATGTAGACTTAGGACAAAATACCAATTC 2884
Db 761 AsnThrAsnValAspLeuGlyAlaLysThrGlnPhe 772

RESULT 2

G86546
 polymorphic outer membrane protein G family [imported] - Chlamydomphila pneumoniae (strain J138)
 C:Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
 C:Accession: G86546
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise, N.
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: G86546
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-928 <STO>
 A:Cross-references: GB:BA000008; MID:98978821; PIDN:BA98657.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: pmp_10
 C:Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Alignment Scores:

Pred. No.: 1.64e-122 Length: 928
 Score: 2058.00 Matches: 444
 Percent Similarity: 61.68% Conservative: 142
 Best Local Similarity: 46.74% Mismatches: 320
 Query Match: 38.05% Indels: 44
 DB: 2 Gaps: 20

US-09-428-122-1 (1-3000) x G86546 (1-928)

QY 101 ATGAAGTCTCTTCCCAAGTTGTATTT---TCTACATTTCTGATTTTC----- 148
 Db 1 MetLysSerGlnPheSerIrpLeuValLeuSerSerThrLeuAlaCysPheThrSerCys 20
 QY 149 CCTTCTCTATGATGCTACCGAGACAGTTTGGATTCAGTGCAGTTTTCGATGGGAAT 208
 Db 21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerAspSerPheAspGlySer 40
 QY 209 AAAAA---CGTAATTTTCAGTTCTGAGAGTCAGAGATGCTGGAACCTACCTACCTA 265
 Db 41 ThrAsnThrGlyThrTyrrProLysAsnThr-----ThrThrGlyIleAspTyrrThr 58
 QY 266 TTTAAGGGAAATGCTACTCTAGAAAATATTCTCGGAACAGGCACACATCAAAAGC 325
 Db 59 LeuThrGlyAspIleThrLeuGlnAsnLeu---GlyAspSerAlaAlaLeuThrLysGly 77
 QY 326 TGTTTTAAACAACACTAAGGGCGATTTGACTTTTACAGGTAACGGGAACCTCTATTGTTT 385
 Db 78 CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyTyrrSerLeuSerPhe 97
 QY 386 CAAACGGTGATCGAGGACTGTAGCAGGGCTGCTGTTTAAACAGCAGCGTGTAGATAAA 445
 Db 98 LeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---SerValThrThrAspLys 115
 QY 446 TCTACACACTTATAGGGTTTCTTCGCTATCTTTTATTGCTCTCTCGAGATTCGATA 505
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 QY 506 ACTACC-----GGCAAGGAGCCGTTAGCTGCTTACGGGTAGCTTGTAGTTTGACAAA 559
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R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
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Best Local Similarity: 46.74% Mismatches: 320
Query Match: 38.05% Indels: 44
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Db 21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerAspSerPheAspGlySer 40
QY 209 AAAAAAT---GGTAATTTTTCAGTTCTGTAGAGTCAAGAAAGATGCTGGAACCTACCTACCTA 265
Db 41 ThrAsnThrGlyThrTyrThrProLysAsnThr-----ThrThrGlyIleAspTyrThr 58
QY 266 TTTAAGGGAAATGTCACTCTAGAAAATATTCTCGAAGACAGGACAGCAATCAAAAAGC 325
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QY 326 TGTTTTAAACACACTAAGGGCGATTGACTTTTACAGGTAACGGGAACCTCTCTATTGTTTC 385
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QY 446 TCTACCAGTTTATAGGTTTCTTCGTATCTTTTATTCGTCTCTCGGAAGTTCGATA 505
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C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: B72077; B81592
R:Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
R.; Kalman, S.; Mitchell, W.; 1999
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: B72077
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R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
R.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
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A:Gene: pmp 9; CP0306
C:Superfamily: Chlamydoiphila pneumoniae polymorphic outer membrane protein G

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```



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Db      451 valLeuArgAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg 470
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1517 CTCGAAATGACGAGTAGGAATCTCTAGAACCTGCTGATACTAGC---ACCATAAACAAT 1573
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      471 IleLeuMetAspGlyGlyThrThrLeuSerAlaLysGluAlaAsnLeuSerLeuAsnGly 490
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1574 TTGGTCATTAACTACGTTCTATAGACGGTGCAAGAGCAAAATAGAAACCAAGCT 1633
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      491 LeuAlaValAsnLeuSerLeuAspGlyThrAsnLysAlaAlaLeuLysThrGluAla 510
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1634 ACGTCAAAAATCTGACTTATCTGGAACCATCACTTTATTTGGACCGACGGCAGCTTT 1693
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      511 AlaAspLysAsnLysSerLeuSerGlyThrIleAlaLeuIleAspThrGluGlySerPhe 530
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1694 TATGAAATCATAGTTTAAAGAAATCCCTACGCTTACGACATCTTAGAGCTCAAA----- 1747
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      531 TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrAla 550
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1748 ---GCTTCTGGAAGTAAAGACCGAGTGAATCCAGATCCATCTATAATGGGTGAGAA 1804
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      551 GlyAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrLeuGlnGluProGlu 570
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1805 TTCATTACCGCTATCAGGGAACCTGGGGCCCAATTGTTGGGGGACAGGGGCTTCTACG 1864
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      571 ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1865 ---ACTGCAACCTCACTCGACTAAACATGGCTATATCTTAATCCCGAGCGTATCGGC 1921
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      590 LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluArgLysSer 609
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1922 TCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTCTCTCCATTATCIT 1981
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      610 AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      1982 ATGGAGACTGCAACGAAGGTTGCGAGGAGACCGTGCTTTTGGTGTGCTGATATCT 2041
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      630 IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla 649
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2042 AACTTCTTCATAGGATAGTACAAACACGACGCGGGTTTCGCCATTTAGTGGCGGT 2101
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      650 AsnPhePheTyrArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGly 669
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2102 TATGTCATAGGAGGAACCTACATCTGTTTCAGATAAGATTCTTAGTGTGCTGATTTGT 2161
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      670 TyrAlaLeuGlyIleThrAlaThrThrProAlaGluAspGlnLeuThrPheAlaPheCys 689
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2162 CAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTACGGA 2221
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      690 GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly 709
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2222 GGAACCTCTATTACAGACACACGAAACCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2275
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      710 AlaSerLeuTyrPheHisIleThrGluGlyLeuPheAspIleAlaAsnPheLeuTrpGly 729
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2276 -----CGGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2323
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      730 LysAlaThrArgAlaProTrpValLeuSerGluIleSerGlnIleIleProLeuSerPhe 749
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2324 TCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAAGTATACCAATAT 2383
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      750 AspAlaLysPheSerTyrLeuHisIleThrAspAsnHisMetLysThrTyrThrAspAsn 769
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2384 CCTACTGTAAAGAGCTGGGGGAATGATAGTTTCGCTTTTAAATTCGGTGAAGAGCT 2443
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      770 SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu 789
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2444 CCGATTTCCTAGATGAAAGTCTCTATTTCAGCAGTACATGCCCTTCATGAATTCGAC 2503
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      790 ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln 809
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2504 TTTGCTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAACTCGTGAATTTGGA 2563
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

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Db      810 TyrIleTyrAlaHisGlnGlnAspPheTyrGluArgHisAlaGluGlyArgAlaPheAsn 829
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2564 AGTAGCGCTTCTGTAATCTTGCTTACCTATCGGATCCGATTTCTATAGAGGAATCAGAC 2623
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      830 LysSerGluLeuIleAsnValGluIleProIleGlyValThrPheGluArgAspSerLys 849
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2624 TGGCAAGATGCAACGATACAACTCTTCTTGGTTATCTATCTGTGGATCTTGTTCGTAGTAAC 2683
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      850 SerGluLysGlyThrTyrAspLeuThrLeuMetTyrIleLeuAspAlaTyrArgAsn 869
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2684 CCGACTGTACGACACACTCGCAATTAGCGGTGATCTTGGAAACCTTCGTACGAAT 2743
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      870 ProLysCysGlnThrSerLeuIleAlaSerAspAlaAsnTrpMetAlaTyrGlyThrAsn 889
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2744 TTGGCAAGCAAGCTTTAGTCTCTGTCAGGGAACCACTTTTGTCTTAACTCAAAATTT 2803
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      890 LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlnValAsnProHisMet 909
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2804 GAAGCCTTTAGCAATTTCTTTTGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2863
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      910 GluIlePheGlyGlnPheAlaPheGluValArgSerSerArgAsnTyrAsnThrAsn 929
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      2864 TTAGGAGCAAAATACCAATTC 2884
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      930 LeuGlySerLysPheCysPhe 936
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

RESULT 7
C86546
polymorphic outer membrane protein G family [imported] - Chlamydothila pneumoniae (str
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: C86546
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491, MUID:20330349; PMID:10871362
A:Accession: C86546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-936 <STO>
A:Cross-references: GB:BA000008; NID:98978817; PIDN:BA098653.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp 7
C:Superfamily: Chlamydothila pneumoniae polymorphic outer membrane protein G

Alignment Scores:
Pred. No.: 1-46e-116 Length: 936
Score: 1964.00 Matches: 411
Percent Similarity: 62.30% Conservative: 179
Best Local Similarity: 43.40% Mismatches: 327
Query Match: 36.31% Indels: 30
DB: 2 Gaps: 16

US-09-428-122-1 (1-3000) x C86546 (1-936)
QY      101 ATGAAGTCTTCTTTCCCAAGTTTGATTTTCTACATTTGCTATTTTC---CCTTTGCT 157
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      1 MetLysSerSerValSerTrpLeuPhePheSerSerIleProLeuPheSerSerLeuSer 20
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      158 ATGATTGCTACGACACAGTTTGGATTCAGT---GGAGTTTCGATGGGAATAAATAAT 214
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      21 IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrAspGlySerAsnGly 40
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      215 GGTAAATTTTTCAGTTTCGTGAGACTCAGGAA---GATGCTGGAACCTACCTACCTATTAAAG 271
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      41 ThrThrPheThrValPheSerThrThrAspAlaAlaGlyThrThrTyrSerLeuLeu 60
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      272 GGAAATGCTACTCTAGAAAATATTCTCTGGAAACAGCAGCAGCAATCAGAAAAGCTGTTT 331
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      61 SerAspValSerPheGlnAsnAlaGlyAlaLeuGlyIleProLeuAlaSerGlyCysPhe 80
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
QY      332 AACACACTAGGGCGGATTTGACTTTCACAGTAACGGGAACCTCTCTATTGTTCCAAACG 391
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

```

431	Db	IleAlaIaAsnValThrSerThrIleArgGlnProAlaValIleuAlaArgGlyAspLeu	450
1457	Qy	TCITTTAAACATGGAGTACTCTGCAGACTCAGGCATTCCTCAACAGGCAGATTCTCGT	1516
451	Db	ValIeuAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg	470
1517	Qy	CTCGAATGACGTAGGACTACTCTAGAACCTGCTGATACTAGC---ACCATATAACAAT	1573
471	Db	IleIeuMetAspGlyGlyThrThrLeuSerAlaIysGluAlaAsnLeuSerLeuAsnGly	490
1574	Qy	TTGGTCATTAACTCAGTCTTATAGACGGTGCAAAGAGCCAAATAATAGAAACCAAGCT	1633
491	Db	LeuAlaValAsnLeuSerSerLeuAspGlyThrAsnIleAlaAlaLeuLysThrGluAla	510
1634	Qy	ACGTCAAAAATCTGACTTTATCTGGAACCATCATTATTGACCCGACGGGACGCTTT	1693
511	Db	AlaAspLysAsnIleSerLeuSerGlyThrIleAlaLeuIleAspThrGluGlySerPhe	530
1694	Qy	TATGAAATCATAGTTTTAAAGAAATCTCAGTCCTACGACATCTTAGAGCTCAAA-----	1747
531	Db	TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrAla	550
1748	Qy	---GCTTCTGGAAGTAAACAGCACCGCAGTACTCCAGATCCTATAATATGGGTGAGAAA	1804
551	Db	GlyAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrLeuGlnGluProGlu	570
1805	Qy	TTCCATTACCGCTATCAGGGAACCTTGGGGCCCAATGTTTGGGGGACAGGGCTTCTACG	1864
571	Db	ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer	589
1865	Qy	---ACTGCAACCTTCACTGGACTAAACTGGCTATATTCCTAAATCCGAGCGGTATCGGC	1921
590	Db	LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluArgLysSer	609
1922	Qy	TCITTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTACTTT	1981
610	Db	AsnLeuProIeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu	629
1982	Qy	ATGAGAGTCTGCAACAGAGGGTTGACGGGAGACCGTCTTTTTGGTGTGTGGATTATCT	2041
630	Db	IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla	649
2042	Qy	AACCTCTTCATAGGATAGTACAAACACGACGCGGGTTCGCCATTTCAGTGGCGGT	2101
650	Db	AsnPhePheTyrArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGly	669
2102	Qy	TATGTCATAGAGGAAACCTACATCTGTTTCAGATAAGATTCCTAGTGTGCACTTTGT	2161
670	Db	TyrAlaLeuGlyIleThrAlaThrThrProAlaGluAspGlnLeuThrPheAlaPheCys	689
2162	Qy	CAGTCTTTGGAAGAGATAGAGACTCTTTGTAGCTAAGATCAAGGTACAGTCTACGGA	2221
690	Db	GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly	709
2222	Qy	GGAACCTCTATTACCAGCAACGAAACCTATATCTCTCTCTCTTGCACAACTA-----	2275
710	Db	AlaSerLeuTyrPheHisHisThrGluGlyLeuPheAspIleAlaAsnPheLeuTrpGly	729
2276	Qy	-----CGCCCTTGTTCGTTGCTTATGTTCTCTACAGAGATTCTGTTCTCTTT	2333
730	Db	LysAlaThrArgAlaProTrpValLeuSerGluIleSerGlnIleIleProLeuSerPhe	749
2324	Qy	TCAGGAAACCTTAGCTACACCCATACGATAAGCATCTGAAACCAAGTATACACATAT	2383
750	Db	AspAlaTyrPheSerTyrLeuHisThrAspAsnHisMetLysThrTyrTyrThrAspAsn	769
2384	Qy	CCTACTCTTAAAGGAAGCTGGGGAATCATAGTTCGTTTTCAGTAATTCGGTGAAGAGCT	2443
770	Db	SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu	789
2444	Qy	CCGATTTCCTAGATGAAGTCTCTATTTCGACAGTACATGCCCTTCATGAATTCGAC	2503
790	Db	ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln	809

Db 411 IleGluTyrGlyGlyAlaIleValPheSerGlyGluLysLeuSerProThrGluLysAla 430
 QY 1397 GATTCTAAATCTTCTGAGAGCTACTACAGCTGTACTTCTTCCAGAGGTACTCTA 1456
 Db 431 IleAlaAlaSerValThrSerThrIleArgGlnProAlaValLeuAlaArgGlyAspLeu 450
 QY 1457 TCTTTAAACATGAGTGACTCTCGACACTCAGGCATCTCAACAGGCGAGATTCTCGT 1516
 Db 451 ValLeuArgAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg 470
 QY 1517 CTCGAAATGGAGCTAGGACTTCTCTAGAACCTCTGATAGC---ACCATAACAAT 1573
 Db 471 IleLeuMetAspGlyGlyThrLeuSerAlaLysGluAlaSerLeuSerLeuAsnGly 490
 QY 1574 TTGGCTCATTTACATCAGTCTATAGACGGTGCAGGCAAGGCAAAATAGAAACCAAGCT 1633
 Db 491 LeuAlaValAsnLeuSerSerLeuAspGlyThrAsnLysAlaLeuLysThrGluAla 510
 QY 1634 ACGTCAAAATCTGACTTTATCGGAACCATCTATTATGGACCGGCGGACAGTTT 1693
 Db 511 AlaAspLysAsnIleSerLeuSerGlyThrIleAlaLeuIleAspThrGluGlySerPhe 530
 QY 1694 TATGAATATCATAGTTAAAGAACTCTCAGTCTACGACATCTTAGAGCTCAAA----- 1747
 Db 531 TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrThrAla 550
 QY 1748 ---GCTTCTGGAATCTTAACAGCACCGCAGTCTCCAGATCCTATAATGGGTGAGAAA 1804
 Db 551 GlyAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrLeuGlnGluProGlu 570
 QY 1805 TTCATTACGCTATCAGGAACTTGGGGCCCAATTTGTTGGGACAGGGGCTTCTACG 1864
 Db 571 ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
 QY 1865 ---ACTGCAACCTTCAACTGACATAAACTGGCTATATCTCAATCCGAGCGTATCGGC 1921
 Db 590 LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluLysSer 609
 QY 1922 TCTTTAGTCCCTATAGCTTATGGATCCATTATAGATATAGTCTCTCTCCATTATCTT 1981
 Db 610 AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629
 QY 1982 ATGGAGACTGCAAAACGAAAGGTTGCGAGGACCGTCTGTTTGGTGTGCGATATCT 2041
 Db 630 IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla 649
 QY 2042 AACTTCTTCCATAGAGATAGACTACTTCTAGCTAAGATCAAGTACAGTCTACGGA 2221
 Db 690 GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly 709
 QY 2222 GGAATCTCTATTACGACGACAGCAACCTATATCTCTCTCTCTGCAACTA----- 2275
 Db 710 AlaSerLeuTyrPheHisThrGluGlyLeuPheAspIleAlaAsnPheLeuTrpGly 729
 QY 2276 -----CGGCTTGTTCGTTGTCTTATGTTCTCAGAGATTCCTGTTCTCTTT 2323
 Db 730 LysAlaThrArgAlaProTrpValLeuSerGluIleSerGlnIleProLeuSerPhe 749
 QY 2324 TCAGGAACCTTAGCTACCCATACGATACGATACGATACGATACGATACGATACGAT 2383
 Db 750 AspAlaLysPheSerTyrLeuHisThrAspAsnHisMetLysThrTyrThrAspAsn 769
 QY 2384 CCTACTGTTAAAGAGAGCTGGGGGATGATAGTTTCGTTTGTAGATTCGGTGGGAAGCT 2443
 Db 770 SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu 789

QY 2444 CCGATTTCCTTATGATGAAGTCTCTATTGACAGCTACATGCCCTTCATGAATTCGAC 2503
 Db 790 ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln 809
 QY 2504 TTTGCTCTATCATCATCAGGAAGTCTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGA 2563
 Db 810 TyrIleTyrAlaHisGlnAspPheTyrGluArgTyrAlaGluGlyArgAlaPheAsn 829
 QY 2564 AGTAGCGCTCTGTAATCTTGCCTTACCTATCCGATCCGATTCGATTAAGGAATCAGAC 2623
 Db 830 LysSerGluLeuIleAsnValGluIleProIleValThrPheGluArgAspSerLys 849
 QY 2624 TGCCAAGATGCAAGTCAACATCTTGGTGTATATCTGTGATCTTGTCTGTAGTAAC 2683
 Db 850 SerGluLysGlyThrTyrAspLeuLeuMetTyrIleLeuAspAlaTyrArgAsn 869
 QY 2684 CCCGACTGTACGACCAACACTGCGAATGAGCGGTGATCTCTGGAACCTTCGTGACGAT 2743
 Db 870 ProLysCysGlnThrSerLeuIleAlaSerAspAlaAsnTrpMetAlaTyrGlyThrAsn 889
 QY 2744 TTGGCAAGACAAAGCTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTAACTCAATTTT 2803
 Db 890 LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlnValAsnProHisMet 909
 QY 2804 GAAGCTTTAGCCAAATTTCTTTGGAATTCGCGGTGATCTCGCAATTCGATAGAC 2863
 Db 910 GluIlePheGlyGlnPheAlaPheGluValArgSerSerArgAsnTyrAsnThrAsn 929
 QY 2864 TTAGGACCAAAATACCAATTC 2884
 Db 930 LeuGlySerLysPheCysPhe 936
 RESULT 9
 D86546
 Polymorphic outer membrane protein G family [imported] - Chlamydomonas pneumoniae (st
 C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
 C:Accession: D86546
 R:Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, P.; Ouchi, K.; Shiba, T.;
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: D86546
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-930 <STO>
 A:Cross-references: GB:BA000008; NID:g8978818; PIDN:BA098654.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G
 Alignment Scores:
 Pred. No.: 4.8e-115 Length: 930
 Score: 1940.00 Matches: 416
 Percent Similarity: 60.97% Conservative: 165
 Best Local Similarity: 43.65% Mismatches: 324
 Query Match: 35.87% Indels: 48
 Gaps: 17
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 QY 101 ATGAAGTCTTCTTCCCAAGTTGTATTTTCTACATTTGCTATTTTCCCTTTCTATG 160
 Db 1 MetLysIleProLeuHisLysLeuLeuIleSerSerThrLeuValThrProIleLeu 20
 QY 161 ---ATTGCTACC-----GAGACAGTTTGTGATTCAGTCGAGTTCGATGGAAT 208
 Db 21 SerIleAlaThrTyrGlyAlaAspAlaSerLeuSerProThrAspSerPheAspGlyAla 40
 QY 209 AAAAATGGTAATTTTTCAGTTTCGTGAGAGTCAGGAAGTCTGGAATCTACCTATTT 268

Db 41 GlyGlySerThrPheThrProLysSerThrAlaAspAlaSerGlyThrAsnTyrValLeu 60
QY 269 AAGGAAATGTCACCTCTAGAAAAATATCTCTGGAACAGCAGCAACATCAAAAAAGCTGT 328
Db 61 SerGlyAsnValTyrIle---AsnAspAlaGlyLysGlyThrAlaLeuThrGlyCysCys 79
QY 329 TTTAAACAACACTAAGGGCGATTTCAGCTTTACAGGTAACGGGAACCTCTATTGTTCCAA 388
Db 80 PheThrGluThrThrGlyAspLeuThrPheThrGlyLysGlyTyrSerPheSerPheAsn 99
QY 389 ACGGTGGATGACAGGACTGTAGCAGGGCTGCTTTAACAGCAGCGTGGTAGATAATCT 448
Db 100 ThrValAspAlaGlySerAsnAlaGlyAlaAlaAla---SerThrThrAlaAspLysAla 118
QY 449 ACCAGCTTTATAGGTTTCTTCGCTATCTTTATGCTCTCTGGAAGTTCGATAACT 508
Db 119 LeuThrPheThrGlyPheSerAsnLeuSerPheIleAlaAlaProGlyThrThrValAla 138
QY 509 ACCGGCAAGGAGCCGTAGCTCTACGGGTAGCTTGAGTTTGACAAAAATGTCACT 568
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QY 569 TTGCTCTTCAGCAAAAATTTCACCGAT-----AATGGGGTGTCTATCACCGCA 619
Db 158 IleLeuPheSerGlnAsnValSerAsnGlnAlaAsnAsnGlnGlyAlaIleThrAla 177
QY 620 AAAAAGCTTTTCAATTAACAGGAGCTACAATGTGCTCTGTTTCTGAAAATPACCTCTCA 679
Db 178 LysThrLeuSerIleSerGlyAsnThrSerSerIleThrPheThrSerAsnSerAlaLys 197
QY 680 AAGAAGGGGAGCATTACAGCTTCGATGCTCCGATGCTTACATCTAGTGAACCAAGGGAA 739
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Db 408 AsnSerProLeuAspTyrSerGlyThrIleValPheSerGlyGlyLysLeuSerAlaAsp 427
QY 1388 GAGGCGGCGAGATTCTTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGA 1447
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QY 1508 GATTCTCTGCTCGAATGAGCTAGGAACCTACTCTAGAACCTGCTGATCTAGCACCATA 1567
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QY 1622 GAAACCAAGCTACGCTCAAAAAATCTGACTTTTATCTGGAACCATCATCTTTATTGACCGC 1681
Db 507 GluThrAlaGlyAlaAsnLysThrIleThrLeuThrSerProLeuValPheGluAspSer 526
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Db 527 SerGlyAsnPheTyrGluSerHisThrIleAsnGlnAlaPheThrGlnProLeuValVal 546
QY 1742 CTCAAAGCTCTC-----GGAACTGTAAACAGCACCGCA 1774
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QY 1775 GTGACTCCAGATCTCTATATGCTGAGAAATTCATTCAGGCTATCAGGGAACCTTGGGCG 1834
Db 567 GlnThrProGluPro-----HisTyrGlyTyrGlnGlyHisTrpGlu 580
QY 1835 CCAATTTGTTGGGGAGCGGCTTCTACGACTGCACTTCACTGAGCACTTAAACTGCGC 1894
Db 581 AlaThrTrpAlaAspThrSerThrAlaLysSerGlyThrMetThrTrpValThrThrGly 600
QY 1895 TATATTCTTAATCCCGAGGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATCATTT 1954
Db 601 TyrAsnProAsnProGluArgAlaSerValValProAspSerLeuTrpAlaSerPhe 620
QY 1955 ATGATATTAGTCTCTCCATTTATCTTATGAGAGCTGCAACGAAGGTTGCGAGGAGAC 2014
Db 621 ThrAspIleArgThrLeuGlnGlnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln 640
QY 2015 CGTGCCTTTTGGTGTCTGATTTATCTAATCTTCTTCCATAGATAGTACAAAAACGCA 2074
Db 641 ArgGlyLeuTrpAlaSerGlyThrAlaAsnPhePheHisLysAspLysSerGlyThrAsn 660
QY 2075 CCGGGGTTTCGCAATTTGAGTGGCGGTATGTCATAGGAGGAACTCATACTTGTTC 2134
Db 661 GlnAlaPheArgHisLysSerTyrGlyTyrIleValGlyLysSerAlaGluAspPheSer 680
QY 2135 GATAAGATCTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2194
Db 681 GluAsnIlePheSerValAlaPheCysGlnLeuPheGlyLysAspLysPheLeu 700
QY 2195 GCTAAGAATCAAGGTACAGTCTCAGGAGGAACCTCTTATTACCAACCAACCAACCTAT 2254
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QY 2255 ATCTCTCTTCTGCAAACTACGCGCTTGT-----TCGTTGCTTTATGTTCTCTCAGAG 2308
Db 721 GlyGlyLeuPro-----MetProSerPheGlySerIleThrAspMetLeuLysAsp 737
QY 2309 ATTCTGTTCTCTTTTTCAGGAAACCTTAGCTACACCCATACGATAACGATCTGAAACCC 2368
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QY	1328	GATTCTGCATCAATATACAGGAACATCATCTTCCAGGAGAAAGTTATCAGAGACA	1387	
Db	408	AsnSerProLeuAspTyrSerGlyThrIleValPheSerGlyGluIysLeuSerAlaAsp	427	
QY	1388	GAGCCGCGAGATCTTAAATACTTACTTCGAAGCTACTACAGCGCTGTAACCTTTTCAGGA	1447	
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QY	1508	GATTCTCGTCTCGAAATCGGAGTAGGAACCTACTCTAGAACCTGCTGATCTAGCACCATTA	1567	
Db	468	GlySerThrLeuLeuMetGlnProGlyThrIysLeuIys--AlaAspThrGluAlaIle	486	
QY	1568	AAC-----AATTGGTGCATTAAACATCAGTCTCTATAGACGGTGCAAAGAGGCCAAATA	1621	
Db	487	SerLeuThrIysLeuValAlaIspSerAlaLeuGluIysAsnIysSerValSerIle	506	
QY	1622	GAACACCAAGCTACGTCAAAATACTGACTTTATCTGGAACCACTACTTTATGGACCCG	1681	
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QY	1682	ACGGGCAGCTTTATGAAATCATAGTITTAAGAAATCCTCAGTCTCAGGACATCTTAGAG	1741	
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QY	1775	GTGACTCCAGATCCTATATGGGTGAGAAATTCATTACGGCTATCAGGAACCTGGGC	1834	
Db	567	GlnThrProGluPro-----HisTyrGlyTyrGlnGlyHisTyrGlu	580	
QY	1835	CCAAATTTGTTGGGGCAGGGGCTTCTACGACTCAACCTTCACTGGACTAAACCTGGC	1894	
Db	581	AlaThrTrpAlaAspThrSerThrAlaIysSerGlyThrMetThrTrpValThrThrGly	600	
QY	1895	TATATCTCTATCCGAGCGTATCGGCTCTTTAGTCCCTAATACCTTATGGAATGCATTT	1954	
Db	601	TyrAsnProAsnProGluArgAlaSerValValProAspSerLeuTrpAlaSerPhe	620	
QY	1955	ATAGATATTAGCTCTCTCCATTCTATTATGAGACTCCAAACGAAAGGGTTTCAGGGAGAC	2014	
Db	621	ThrAspIleArgThrLeuGlnGlnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln	640	
QY	2015	CGTCTTTTTCGTGCTGGATTATCTAACCTTCTCCATAGGATAGTACAAAACACGA	2074	
Db	641	ArgGlyLeuTrpAlaSerGlyThrAlaAsnPheHisTyrAspLysSerGlyThrAsn	660	
QY	2075	CGCGGGTTTCGCCATTTGAGTGGCGGTATTCTCATAGGAGAAACCTACATACCTGTGTCA	2134	
Db	661	GlnAlaPheArgHisLysSerTyrGlyTyrIleValGlySerAlaGluAspPheSer	680	
QY	2135	GATPAGATTTCTAGTCGTGCATTTTGTGACGCTCTTTTGGAGAGATAGAGACTCTTTGTA	2194	
Db	681	GluAsnIlePheSerValAlaPheCysGlnLeuPheGlyIysAspLysAspLeuPheIle	700	
QY	2195	GCTAAGAAATCAAGGTACAGTCTCAGGAGAACTCTCTATTACCAGCACCAACGAAACCTAT	2254	
Db	701	ValGluAsnThrSerHisAsnTyrLeuAlaSerLeuTyrLeuGlnHisArgAlaPheLeu	720	
QY	2255	ATCTCTCTTCTCTGCAAACTACGGCCTTGT-----TCGTTGTCTTATGTTCTCACAG	2308	
Db	721	GlyGlyLeuPro-----MetProSerPheGlySerIleThrAspMetLeuLysAsp	737	

Qy 2309 ATTCTGTTCTCTTTCAGGAACCTTAGCTACACCCATACGGATACGACTGTGAAACC 2368
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| | | | : : : : : : | | | | : : : : : : | | | | : : : :
Qy 2369 AAGTATACAAACATATCTACTGTATAAGGAAGCTGGGGAATCATAGTTTCGTCTTAAGA 2428
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Db 758 ArgTyThrSerTyProGluAlaGlnGlySerTipThrAsnAsnSerGlyAlaLeuGlu 777
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RESULT 11
D72078
Polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CML029)
C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C/Accession: D72078
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; MUID:99206606; PMID:10192388
A/Accession: D72078
A>Status: Preliminary
A/Molecule type: DNA
A/Cross-references: 1-930 <ARN>
A/Experimental source: strain CML029
C/Genetics:
A/Gene: pmp 8
A/Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

[illegible]

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Qy	1271	---ACTACAGATCATCCACAACAGTTACAGATGTCTTAAAGCTTAATGAGACTCCGGCA	1327
Db	392	AsnThrThryAlaSer-----AspValIleuThrIleAsnGlnProAspSer	407
Qy	1328	GATTCTGCATCAATATACAGGAAACATCTTTCACAGAGAGAAAAGTTATCAGAGACA	1387
Db	408	AsnSerProLeuAspTyrSerGlyThrIleValPheSerGlyGluLysLeuSerAlaAsp	427
Qy	1388	GAGGCCGCGATTTAAAAATCTTACTTCCGAAGCTACTACAGCGCTGTAACTCTTCAGGA	1447
Db	428	GluAlaLysAlaAlaAspAsnPheThrSerIleLeuLysGlnProLeuAlaLeuAlaSer	447
Qy	1448	GGTACTCTATCTTTAAACAATGAGTAGTCTCTCAGACTCAGGCATTCTCAACAGGCA	1507
Db	448	GlyThrLeuAlaLeuLysGlyAsnValGluLeuAspValAsnGlyPheThrGlnThrGlu	467
Qy	1508	GATTCTCGTCTCGAAATGAGCTAGGAATCTACTCTAGAACTCTCTATACACTAGCACCAT	1567
Db	468	GlySerThrLeuLeuMetGlnProGlyThrLysLeuLys---AlaAspThrGluAlaIle	486
Qy	1568	AAC-----AATTTGGTCATTAACATCAGTTCATAGACGGTCCAAAGAGGCAAAATA	1621
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Qy	1622	GAACCAAAAGCTAGCTCAAAAATCTGACTTTATCTGGAACCATCATCTTATTGGACCG	1681
Db	507	GluThrAlaGlyAlaAsnLysThrIleThrLeuThrSerProLeuValPheGlnAspSer	526
Qy	1682	ACGGGACGTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTCAGACATCTTAGAG	1741
Db	527	SerGlyAsnPheTyrGluSerHisThrIleAsnGluAlaPheThrGlnProLeuValVal	546
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Qy	1775	GTGACTCCAGATCCTATAATGGGTGAGAAATCCATTACCGCTATCAGGGAATCTGGGC	1834
Db	567	GlnThrProGluPro-----HisTyrGlyThrGlnGlyHisTrpGlu	580
Qy	1835	CCAATGTGTTGGGGACAGCGGCTTTCAGACTGCACCTTCACTGGACTCAAACTGGC	1894
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Qy	1895	TATATTCTTAATCCGAGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATT	1954
Db	601	TyrAsnProAsnProGluAArgAlaSerValValProAspSerLeuTrpAlaSerPhe	620
Qy	1955	ATAGATATTAGCTCTCCATTATCTTATGGAGACTGCACCAAGAGGTTTCAGGGAGAC	2014
Db	621	ThrAspIleArgThrLeuGlnGlnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln	640
Qy	2015	CGTGCTTTTGGTGTGCTGATATCTAATCTTCTCCATAGAGATAGTACAAAACACGA	2074
Db	641	ArgGlyLeuTrpAlaSerGlyThrAlaAsnPhePheHisLysAspLysSerGlyThrAsn	660
Qy	2075	CGCGGTTTCGCCATTTGAGTGGGGTTATGTCTATAGGAGAACTTACATCTTGTTCA	2134
Db	661	GlnAlaPheArgHisLysSerTyrGlyTyrIleValGlySerAlaGluAspPheSer	680
Qy	2135	GATAAGATTCTTACTGCTGCATTTTGTGACCTCTTTGGAGAGATAGACTACTTGTA	2194
Db	681	GluAsnIlePheSerValAlaPheCysGlnLeuPheGlyLysAspLysAspLeuPheIle	700
Qy	2195	GCTAAGATCAAGGTACAGTCTACGGAGGAACCTCTATTACCAGCACACGAACCTAT	2254
Db	701	ValGluAsnThrSerHisAsnTyrLeuAlaSerLeuTyrLeuGlnHisArgAlaPheLeu	720
Qy	2255	ATCTCTCTTCTCCAAACTACGGCCCTGT-----TCGTTGTCTTATGTTCTCTACAG	2308

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QY      2369 AAGTATACAAATATCTCTACTGTTTAAAGGAGCTGGGGAATGATAGTTTGGCTTTAGAA 2428
Db      758 ArgTyrThrSerTyrProGluAlaGlnGlySerTyrThrAsnAsnSerGlyAlaLeuGlu 777
QY      2429 TTCGGTGAAGAGCTCCGATTTGCTTAA---GATGAAAGTGTCTTATTTGACGAGTACATG 2485
Db      778 LeuGlyGlySerLeuAlaLeuTyrLeuProLysGluAlaProPhePheGlnGlyTyrPhe 797
QY      2486 CCCTTCATGAATTCGATTTGCTATGACATCAGGAAGTTTAAAGAACAGGGAACA 2545
Db      798 ProPheLeuLysPheGlnAlaValTyrSerArgGlnGlnAsnPheLysGluSerGlyAla 817
QY      2546 GAAGCTCGTGAATTTGGAAGTAGCGCTTCTGTGAATCTTGCTTACCTATCGGATCCGA 2605
Db      818 GluAlaArgAlaPheAspAspGlyAspLeuValAsnCysSerIleProValGlyLeArg 837
QY      2606 TTGATGAAGAAATCAGACTGCCAAGATGCCAAGTACAAATCTAATCTTGTGTTACTGTG 2665
Db      838 LeuGluLysIleSerGluAspGluLysAsnAsnPheGluIleSerLeuAlaTyrIleGly 857
QY      2666 GATCTTGTTCGTAGTACCCGACTGACGACAACTGCGAATACCGGTGATCTTTGG 2725
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QY      2726 AAAACCTTCGCTACGAATTTGGCAAGACAAGCTTTAGTCTCTCGTCAGGGAACCAATTT 2785
Db      878 ThrSerLeuLysLysAsnLeuAlaArgGlnAlaPheLeuAlaSerAlaGlySerHisLeu 897
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QY      2846 CGCAATTTACAAATTTAGCTTAGGAGCAAAATACCAATTC 2884
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RESULT 12
F81591
polymorphic membrane protein G family CP0302 [imported] - Chlamydomphila pneumoniae (stra
C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C;Accession: F81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-949 <REA>
A;Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38159.1; PID:g718922
A;Experimental source: strain AR39, HU cells
C;Genetics:
A;Gene: CP0302
C;Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Alignment Scores:
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Score: 1868.00 Matches: 412
Percent Similarity: 60.49% Conservative: 176
Best Local Similarity: 42.39% Mismatches: 334
Query Match: 34.54% Indels: 50
DB: 2 Gaps: 22

US-09-428-122-1 (1-3000) x F81591 (1-949)

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 C:Accession: E72130; G81541
 R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72000; MUID:99206606; PMID:10192388
 A;Accession: E72130
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 A;Experimental source: strain CWL029
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke

C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A; Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.
 A; Reference number: AB1500; MUID:20150255; PMID:10684935

A; Accession: G81541
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 A; Cross-references: GB:AE002235; GB:AE002161; MID:g7189672; PIDN:AAF38561.1; PID:g718967
 A; Experimental source: strain AR39, HL cells
 C; Genetics:

A; Gene: pmp_2; CP0761
 C; Superfamily: Chlamydothila pneumoniae polymorphic outer membrane protein G

Alignment Scores:

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US-09-428-122-1 (1-3000) x E72130 (1-841)

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 DB 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val 386
 QY 1550 GCTGATCTAGCACCTATA-----ACAAATTGGTCAATTAACATCAGTCTCTATAGCGGT 1603
 DB 387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAen 406
 QY 1604 GCAAGGAAGCAAAATAGAAACCAAGCTACGTCAAAATCTGACTTTATCTGGAACC 1663
 DB 407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
 QY 1664 ATCACTTTATGGACCGCGGCGCGCTTTTATGAAATCATATAGTTTAAAGAAATCTCTAG 1723
 DB 427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
 QY 1724 TCCTACGAC---ATCTTAGAGCTCAAGCTTCTGGAACCTGTAACAGCACCGCGAGTACT 1780
 DB 447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla---Asp 466
 QY 1781 CCAGATCTTAATGGTGGAGAAATTCATTCAGCTATCAGGAACTTGGGGCCCAATT 1840
 DB 466 erArgSerIleAspAlaValGlnSerPro-TyrGlyTy-GlnGlyLysTrp---ThrIle 484
 QY 1841 GTTTGGGGGACAGGGGCTTCTACAGTGCACCTCACTGGACTAAAAGTGGCTATATT 1900
 DB 485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAen 503
 QY 1901 CCTAATCCGAGGCTATCGGCTCTTTAGTCCCTTAATAGTCTTATGGAATGATGATTTATAGAT 1960
 DB 504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523

Search completed: December 16, 2003, 10:33:17
Job time : 142.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 16, 2003, 10:21:33 ; Search time 27.5 Seconds
(without alignments)
10260.372 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 5409
Sequence: 1 cgccttactctagtaggt.....tggttgtctaaacactttc 3000

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=US09428122.spool p/US09428122/runat 16122003 102127 10766/app_query.fasta_1.3143
-DB=SwissProt 41 -QPMF=fastan -SUFFIX=rsb -MINMATCH=0.1 -IOOPCI=0 -IOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09428122 @CGN 1 1 32 @runat.16122003 102127 10766 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2058	38.0	928	PM10_CHLNP	Q9rb55 chlamydia p
2	1982	36.6	928	PM10_CHLNP	Q92398 chlamydia p
3	1964	36.3	936	PM10_CHLNP	Q92898 chlamydia p
4	1936	35.8	930	PM10_CHLNP	Q92393 chlamydia p
5	1855	34.3	928	PM11_CHLNP	Q86164 chlamydia p
6	1580.5	29.2	841	PM10_CHLNP	Q923a1 chlamydia p
7	1444	26.7	1276	PM10_CHLNP	Q92899 chlamydia p
8	1442.5	26.7	922	PM10_CHLNP	Q92895 chlamydia p
9	1377.5	25.5	973	PM10_CHLNP	Q92896 chlamydia p
10	1120.5	20.7	1013	PM10_CHLNP	Q92897 chlamydia p
11	1051	19.4	987	PM10_CHLNP	Q92898 chlamydia p
12	911	16.8	867	PM10_CHLNP	Q92899 chlamydia p
13	863	16.0	878	PM10_CHLNP	Q92895 chlamydia p
14	685.5	12.7	1609	PM10_CHLNP	Q92896 chlamydia p
15	667.5	12.3	978	PM10_CHLNP	Q92895 chlamydia p
16	666	12.3	947	PM10_CHLNP	Q92896 chlamydia p
17	666	12.3	1723	PM10_CHLNP	Q92895 chlamydia p
18	665.5	12.3	946	PM10_CHLNP	Q92896 chlamydia p

19	650.5	12.0	952	1	PM16_CHLNP	Q92882 chlamydia p
20	605.5	11.2	975	1	PM16_CHLNP	Q84417 chlamydia t
21	604.5	11.2	938	1	PM15_CHLNP	Q92883 chlamydia p
22	597	11.0	1016	1	PM16_CHLNP	Q84880 chlamydia t
23	594	11.0	980	1	PM16_CHLNP	Q9p144 chlamydia m
24	590.5	10.9	976	1	PM16_CHLNP	Q9p143 chlamydia m
25	576.5	10.7	1531	1	PM16_CHLNP	Q84818 chlamydia t
26	559	10.3	1754	1	PM16_CHLNP	Q84418 chlamydia t
27	549.5	10.2	976	1	PM16_CHLNP	Q9p147 chlamydia m
28	548.5	10.1	1672	1	PM16_CHLNP	Q9p142 chlamydia m
29	544	10.1	1520	1	PM16_CHLNP	Q9p146 chlamydia m
30	541.5	10.0	984	1	PM16_CHLNP	Q84877 chlamydia t
31	533.5	9.9	1460	1	PM16_CHLNP	Q9p141 chlamydia m
32	523	9.7	1770	1	PM16_CHLNP	Q84419 chlamydia t
33	490	9.1	1034	1	PM16_CHLNP	Q92882 chlamydia p
34	475.5	8.8	514	1	PM12_CHLNP	Q923d6 chlamydia t
35	454	8.4	1025	1	PM16_CHLNP	Q9p146 chlamydia m
36	269	5.0	2249	1	PM16_CHLNP	Q92882 chlamydia p
37	251	4.6	2021	1	PM16_CHLNP	Q92882 chlamydia p
38	238.5	4.4	1025	1	PM16_CHLNP	Q92882 chlamydia p
39	237.5	4.4	881	1	PM16_CHLNP	Q92882 chlamydia p
40	234	4.3	1645	1	PM16_CHLNP	Q92882 chlamydia p
41	233.5	4.3	1609	1	PM16_CHLNP	Q92882 chlamydia p
42	232	4.3	1643	1	PM16_CHLNP	Q92882 chlamydia p
43	230	4.3	995	1	PM16_CHLNP	Q92882 chlamydia p
44	230	4.3	1250	1	PM16_CHLNP	Q92882 chlamydia p
45	228	4.2	3178	1	PM16_CHLNP	Q92882 chlamydia p

ALIGNMENTS

RESULT 1
PM10_CHLNP
ID PM10_CHLNP STANDARD; PRT; 928 AA.
AC Q9RB65; Q86163; Q9RB64; Q9S6P2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmpl0 precursor (Polymorphic membrane protein 10) (Outer membrane protein 5).
GN PM10 OR OMP5 OR CP0303.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.,
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity.",
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.,
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.",
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA.",

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RL Nucleic Acids Res. 28:2311-2314 (2000).
RN [4]
RP SEQUENCE OF 1-914 FROM N.A.
RC STRAIN=OWL029/VR-1310;
RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
RT membrane proteins of Chlamydia pneumoniae.";
RT Infect. Immun. 67:375-383 (1999).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL)
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AJ133034; CAB37071.1; -
CC DR EMBL: AE002192; AAF38160.1; -
CC DR EMBL: AP002546; BAA98657.1; -
CC DR EMBL: AJ001311; CAA04671.1; -
CC DR PIR: G81591; G81591.
CC DR PIR: G86546; G86546.
CC DR PHCI-2DPAGE; O86163; -.
CC TIGR: CP0303; -.
CC InterPro: IPR006315; Autotransport.
CC DR InterPro: IPR003368; Chlamydia_PMP.
CC DR Pfam: PF02415; DUF145; 2.
CC DR TIGRFAMS: TIGR01414; autotrans_bar1; 1.
CC DR TIGRFAMS: TIGR01376; POMP repeat; 6.
CC KW Outer membrane; Signal; Multigene family.
CC FT SIGNAL 1 25 POTENTIAL.
CC FT CHAIN 26 928 PROBABLE OUTER MEMBRANE PROTEIN PMP10.
CC SQ SEQUENCE 928 AA; 97229 MW; 0590D5206A1DD0E1 CRC64;

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Alignment Scores:

Pred. No.:	2-22e-116	Length:	928
Score:	2058.00	Matches:	444
Percent Similarity:	61.68%	Conservative:	142
Best Local Similarity:	46.74%	Mismatches:	320
Query Match:	38.05%	Indels:	44
DB:	1	Gaps:	20

US-09-428-122-1 (1-3000) x PMP10_CHLPP (1-928)

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DB 1 MetLysSerGlnPheSerTrpLeuValLeuSerSerThrLeuAlaCysPheThrSerCys 20
QY 149 CCTTTCTCTATGATTCCTACCGAGACAGTTTTCGATTCAGTCGAGTTTCGATGGGAAT 208
DB 21 SerThrValPheAlaThrAlaGluAsnIleGlyProSerAspSerPheAspGlySer 40
QY 209 AAAAAAT---GGTAATTTTTCAGTCGTGAGAGTCAGGAAGATGCTCGAACTACCTACTTA 265
DB 41 ThrAsnThrGlyThrThrProLysAsnThr-----ThrThrGlyIleAspThrThr 58
QY 266 TTTAAGGGAATGCTACTAGAAAATATTCCTGGAAACAGGCACACATATCAAAAAGC 325
DB 59 LeuThrGlyAspIleThrGluInAsnLeu---GlyAspSerAlaAlaLeuThrLysGly 77
QY 326 TGTTTTAAACAACAAAGGCGATTTGACTTTTCACAGGTAACGGGAACTCTCTATTGTTTC 385
DB 78 CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyThrSerLeuSerPhe 97
QY 386 CAAACCGTGATGTCAGGAGCTGTAGCAGGCGTCTGTTTAAACAGCAGCGTGGTAGATAAA 445
DB 98 LeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---SerValThrThrAspLys 115

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446 TCTACCAGTTTATAGGTTTCTTCGTATCTATCTTTTATTCGTCTCTCTGGAAGTTTCGATA 505
 116 AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAProSerSerValIle 135
 506 ACTACC-----GGCAAGAGGCGCTTAGCTCTCTACGGGTAGCTTACGTTTGCACAAA 559
 136 ThrThrProSerGlyLysGlyAlaValLysCysGly---GlyAspLeuThrPheAspAsn 154
 560 AATGTCAGTTTGTCTCTCAGCAAAAACCTTTTCAACGGATAATGGGGTCTATCACCGCA 619
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 175 LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyAsnLysSerSer 194
 680 -----AGAAAGGCGGAGCCATTCAGACTTCCGATCCGATCCCTTACCATCTACGAAAC 730
 195 AlaThrGlyLysLysGlyGlyAlaIleCysAlaThrGlyThrValAspIleThrAsnAsn 214
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 215 ThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaAlaGlyGlyAlaIleAsnSer 234
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 851 GGAGGAGCTCTCTCAACAACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATATAAACT 910
 255 -----AlaThrAlaGly-----AsnGlyGlyAlaLeu----- 263
 911 AGTACAGATACCTAAGGTCACTCCCTCACTGGAATCAGATGTTTACTCTTCAGCAACAATACA 970
 264 SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThrPheSerGlyAsnGln 283
 971 TCGCAACACGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTCGCTGCTCC-----GGA 1024
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 304 GlyGlyIleSerPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyAla 323
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 384 AspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLysAla 403
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 404 AspAlaGlyAsnSerThrAspThrSerGlySerIleValPheSerGlyGlyLysLeuSer 423
 1382 GAGACAGAGGCGGAGATTCTAAAATCTTCTCGAAGCTACTACAGCTGTAACTCTT 1441
 424 GluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLysGlnProValThrLeu 443
 1442 TCAGGAGGTACTCTTCTTTAAACATGGAGTACTCTGCACTACAGCACTTCACTCAA 1501
 444 ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln 463
 1502 CAGGAGATCTCTGCTCTCGAATGACGAGTACTCTAGAACCTGCT---GATACT 1558

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Db 464 ThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu 483
QY 1559 AGCACCATAAACAATTGGTCATTAACTACATCACTTATAGACGGTGCAGAAAGACGCAAAA 1618
Db 484 ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyValVal 503
QY 1619 ATAGAAACCAAGCTACGTCAAAAATCTGACTTTATCTGGAACCATCTTTATTTGGAC 1678
Db 504 IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeuAsp 523
QY 1679 CGACGGGCACGCTTTATGAAATCATAGTTTAAAGAAATCTTCAGTCTCCTACGACATCTTA 1738
Db 524 AsnGlnGlyAsnAlaTyGlnAsnHisAspLeuGlyLysThrGlnAspSerPheVal 543
QY 1739 GAGCTCAAGCTCTTGGAACTGTAAACAGCAGCAGTCACTCCAGATCCCTATAATGGGT 1798
Db 544 GlnLeuSerAlaLeuGlyThrAlaThrThrAspValProAlaValProThrValAla 563
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Db 564 ThrProThrHisTyrglyTyrglnGlyThrTrpGly---MetThrTrpValAspThr 582
QY 1847 ---GGGACACAGGGCTCTACGACTGCAACCTTCAACTGGACTAAACTGGCTATATCT 1903
Db 583 AlaSerThrProLysThrLysThrAlaThrLeuAlaThrThrAsnThrGlyTyzLeuPro 602
QY 1904 AATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGAAATGCAATTTATAGATAT 1963
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QY 1964 AGCTCTCTCCATTATCTTATGAGACTGCAACAGGAAGGGTTCACGGGAGAGCGTCTTT 2023
Db 623 GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuLysCysSerAspArgGlyPhe 642
QY 2024 TGGTGTGCTGGATTACTAACTTCTTCCATAGGATAGTACAAAACACGACGGGTTT 2083
Db 643 TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGlyGluLysArgLysTy 662
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QY 2144 CTTAGTGTCTGATTTTGTACGCTCTTTGAGAGAGATAGAGACTACTTTGTAGCTAAGAT 2203
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Db 703 HisThrAspThrTyAlaGlyAlaPheTyrlleGlnHis-----IleThrGlu 718
QY 2264 CTTGCCAACTACGGCTTGTGCTGTTGCTTATGTTCTCT-----ACAGAGATTCCT 2314
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Db 739 LeuValLeuGluGlyGlnLeuAlaTySerHisValSerAsnAspLeuLysThrLysTy 758
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Db 759 ThrAlaTyProGluValLysGlySerTrpGlyAsnAsnAlaPheAsnMetMetLeuGly 778
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Db 799 LysLeuAsnLeuThrTyrlleArgGlnAspSerPheSerGluLysGlyThrGluGlyArg 818
QY 2555 GAAATTGGAAGTAGCGCTTGTGTAATCTTGCTTACCTATCGGATCCGATTCGATTAAG 2614
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QY 2615 GAATCAGACTGCCAAGATGCAACGTAACATCTAATCTTGTGTATATCTGTGATCTGT 2674
Db 839 PheSerAspCysAsnAspPheSerTyAspLeuThrLeuSerTyValProAspLeuIle 858
QY 2675 CGTAGTAAACCCGACTGTACGACACACTGCGAATAGCGGTGATCTTGTGAAACCTTC 2734
Db 859 ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTy 878
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QY 2855 AATGTAGACTTAGGAGCAAAATACCAATTC 2884
Db 919 AsnValAspLeuGlyGlyLysPheGlnPhe 928

RESULT 2
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AC Q92398;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable outer membrane protein pmp9 precursor (Polymorphic membrane
protein 9) (Outer membrane protein 10).
GN PMP9 OR OMP10 OR CPN0447 OR CP0306.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Bossen T., Hjerno K., Daugaard L., Mygind P.,
Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20030349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
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Db      531  TyrlGluAsnHisLeuLysSerAlaSerThrTyProLeuLeuGluLeuThrAla 550
QY      1748  ---GCTCTGGACGTAAACAGCACCAGCAGTACCTCCAGATCCCTATATGGTGGAGAAA 1804
Db      551  GlyAlaAsnGlyThrLeuLeuGlyAlaLeuSerThrLeuLeuGlnGluProGlu 570
QY      1805  TTCCATTAGCGGTATCAGGGAACCTTGGGGCCCAATTTGGGGACAGGGGCTTCTACG 1864
Db      571  ThrHisTyGlyTyGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
QY      1865  ---ACTGCAACCTTCAACTGGACTAAACTGGCTATATTCCTTAATCCCGAGGTATCGGC 1921
Db      590  LysIleGlySerIleAsnTrpThrArgThrGlyTyIleProSerProGluArgLysSer 609
QY      1922  TCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTATAGATATAGTCTCTCCATATCTT 1981
Db      610  AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629
QY      1982  ATGGAGACTGCAAAACGAAGGGTTGCAGGAGACCGTCTTTTGGTGTGCTGGATTATCT 2041
Db      630  IleGluThrLysSerSerGlyGluProPheGluArgGluLeuTrpLeuSerGlyIleAla 649
QY      2042  AACTTCTTCCATAGGATAGTACAAAACACAGACCGGGTTTCGCCATTTGAGTGGCGGT 2101
Db      650  AsnPhePheTyArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGly 669
QY      2102  TATGTCATAGAGGAAACCTACATCTTGTTCAGATAGATCTTAGTGTGCTGCTATTTGT 2161
Db      670  TyrlAlaLeuGlyIleThrAlaThrProAlaGluAspGlnLeuThrPheAlaPheCys 689
QY      2162  CAGTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAACTCAAGGTACAGTCTACGGA 2221
Db      690  GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyGly 709
QY      2222  GGAATCTCTATTACAGCAACAAACCTATATCTCTCTCTCTGCAAACTA----- 2275
Db      710  AlaSerLeuTyPheHisHisThrGluGlyLeuPheAspIleAlaAsnPheLeuTrpGly 729
QY      2276  -----CGGCCCTTGTTCGTTCTTATGTTCTCTACAGATATCTCTGTTCTCTTT 2323
Db      730  LysAlaThrArgAlaProTrpValLeuSerGluLeuSerGlnIleIleProLeuSerPhe 749
QY      2324  TCAGAAACCTTAGCTACACCATACGATACAGTCTGAAACCAAGTATACACATAT 2383
Db      750  AspalalysPheSerTyLeuHisThrAspAsnHisMetLysThrTyThrAspAsn 769
QY      2384  CCTACTGTTAAGGAAGCTGGGGAAATGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCT 2443
Db      770  SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAlaAspLeuGlyAlaSerLeu 789
QY      2444  CCGATTTGCTTAGATGAAGTGCTCTATTTCAGCAGTACATGCCCTTCATGAAATTCGAG 2503
Db      790  ProPheValIleSerValProTyLeuLeuLysGluValGluProPheValLysValGln 809
QY      2504  TTTGCTATGCATCAGGAAGGTTTAAAGAACAGAGGAAACAGAGCTCGTGAATTTGGA 2563
Db      810  TyrlleTyAlaHisGlnAspPheTyGluArgTyAlaGluGlyArgAlaPheAsn 829
QY      2564  AGTAGCGCTTGTGAATCTTTCCTTACCTATCCGATCCGATGATGATGAAGGAATCAGAC 2623
Db      830  LysSerGluLeuIleAsnValGluIleProIleGlyValThrPheGluArgAspSerLys 849
QY      2624  TGCCAAGATGCAAGTCAACTACTCTTGGTTATCTAGTGGATCTTGTTCGTAGTAAC 2683
Db      850  SerGluLysGlyThrTyAspLeuThrLeuMetTyrlleLeuAspAlaTyArgAsn 869
QY      2684  CCCGACTGTACGCAACACTCGAATAGCGGTGATCTTGGAAACCTTCGGTACCAAT 2743
Db      870  ProlysCysGlnThrSerLeuIleAlaSerAspAlaAsnTrpMetAlaTyGlyThrAsn 889
QY      2744  TTGCAAGACAGACTTTTATGCTCTTCGTGCGAGGGAACCATTTTTCCTTAACCTCAAAATTT 2803

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Db      890  LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlnValAsnProHisMet 909
QY      2804  GAAGCCTTTAGCCCAATTTCTTTGAATGGTGGTGGTCAATCTCGCAATTAACAATGAC 2863
Db      910  GluTrlePheGlyGlnPheAlaPheGluValArgSerSerArgAsnTyrlAsnThrAsn 929
QY      2864  TTAGAGCAAAATACCAATTC 2884
Db      930  LeuGlySerLysPheCysPhe 936

RESULT 4
PMP8 CHLPN
ID_PMP8 CHLPN STANDARD; PRT; 930 AA.
AC 092393; Q3RB66;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
DE protein 8) (Outer membrane protein 11).
GN PMP8 OR OMP11 OR CPN0446 OR CP0307.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
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RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity".
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=39206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.".
RL Nat. Genet. 21:385-389(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read I.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.".
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.".
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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DR EMBL; AJ133034; CAB37068.1; -
DR EMBL; AB001627; AAD18590.1; -
DR EMBL; AB002193; AAF38164.1; -
DR EMBL; AF002546; BAA98654.1; -
DR PIR; A81591; A81591.
DR PIR; D72078; D72078.
DR PHCI-2DPAGE; Q92393; -
DR TIGR; CP0307; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; DUF145; 2.
DR TIGRfams; TIGR01414; autotrans_bar1; 1.
DR TIGRfams; TIGR01376; POMP repeat; 6.
DR Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 930 PROBABLE OUTER MEMBRANE PROTEIN PMP8.
FT CONFLICT 177 177 T -> A (IN REF. 3 AND 4).
SQ SEQUENCE 930 AA; 97669 MW; 46A9B5EBB913C4C CRC64;

Alignment Scores:
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Score: 1936.00 Matches: 415
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Best Local Similarity: 43.55% Mismatches: 325
Query Match: 48 Indels: 48
DB: 1 Gaps: 17

US-09-428-122-1 (1-3000) x PMP8_CHLPP (1-930)
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Db 1 MetCysIleProLeuHisLysLeuLeuSerSerThrLeuValThrProIleLeuLeu 20
QY 161 ---ATTGCTACC-----GAGACAGTTTTTCGATTTCAGTCGCGATTCGGAAT 208
Db 21 SerIleAlaThrThrGlyAlaAspAlaSerLeuSerProThrAspSerPheAspGlyAla 40
QY 209 AAAAATGGTAATTTTCAGTTCGTGAGTCAGAGACAGATGCTGGAAGTACCTACCTATTT 268
Db 41 GlyGlySerThrPheThrProLysSerThrAlaAspAlaAsnGlyThrAsnTyrValLeu 60
QY 269 AAGGGAATCTACTCTAGAAATATCTCGGACAGGACAGACATCAAAAAGCTGT 328
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QY 329 TTTTAAACAACACTAAGGCGGATTTGACTTTTCACAGGTAAACGGGAACCTCTATTGTTCCAA 388
Db 80 PheThrGluThrThrGlyAspLeuThrPheThrGlyLysGlyTyrSerPheSerPheAsn 99
QY 389 ACCGTGATGACGGAGCTGTAGCAGGGCTGCTGTTAAACAGCAGCGTGGTAGATAATCT 448
Db 100 ThrValAspAlaGlySerAsnAlaGlyAlaAlaAla---SerThrThrAlaAspLysAla 118
QY 449 ACCACGTTTATAGGTTTCTTCGCTATCTTTTATTGCGCTCTCTGGAAGTTTCGATACT 508
Db 119 LeuThrPheThrGlyPheSerAsnLeuSerPheIleAlaAlaProGlyThrThrValAla 138
QY 509 ACCGCAAAAGGACCGTGTAGCTGCTCTACGGGTAGCTTGAGTTTGCACAAAATGTCAGT 568
Db 139 SerGlyLysSerThrLeuSer---SerAlaGlyAlaLeuAsnLeuThrAspAsnGlyThr 157
QY 569 TTCTCTCTGACAAAACCTTTCAACGGAT-----AATGGCGGTCTATCACCGCA 619
Db 158 IleLeuPheSerGlnAsnValSerAsnGlnAlaAsnAsnAsnGlyGlyAlaIleThrThr 177
QY 620 AAAACTCTTTTCAATTAACAGGACTACAATGTCAGCTCTGTTTCTGAAATACCTCTCA 679
Db 178 LysThrLeuSerIleSerGlyAsnThrSerSerIleThrPheThrSerAsnSerAlaLys 197
QY 680 AAGAAAGGCGGAGCCATTTCAGACTTCGATGCCCTTACCATTACTGGAACACCAAGGGAA 739
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Db 198 LysLeuGlyGlyAlaIleTyrSerSerAlaAlaAlaSerIleSerGlyAsnThrGlyGln 217
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Db 218 LeuValPheMetAsnAsnLysGlyGluThrGlyGlyGlyAlaLeuGlyPheGluAlaSer 237
QY 800 GTGACTATTTCTAAATCTAAAGTTTCTTTTATGCAATAAGGTACACAGGACGAC 859
Db 238 SerSerIleThrGlnAsnSerLeuPhePheSerGlyAsnThrAlaThrAspAlaAla 257
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Db 272 ProThrLeuThrIleSerGlyAsnLysSerLeuThrPheAlaGluAsnSerSerValThr 291
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QY 1271 ---ACTACAGATCATCCACAACAGTTACAGATGTCTTAAAGTTTAATGAGTCTCGGCA 1327
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Db 507 GluThrAlaGlyAlaAsnLysThrIleThrLeuThrSerProLeuValPheGlnAspSer 526
QY 1682 ACGGCGACGTTTATGAAATCATAGTTTAAAGATCTCTAGTCTCTCAGTCTCAGACATCTTAG 1741
Db 527 SerGlyAsnPheTyrGluSerHisThrIleAsnGlnAlaPheThrGlnProLeuValVal 546
QY 1742 CTCAAAGCTTCT-----GGAACTGTAAACAGCACCGCA 1774
Db 547 PheThrAlaAlaThrAlaAlaSerAspIleTyrIleAspAlaLeuLeuThrSerProVal 566

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QY 1775 GTGACTCCAGATCTATATGGGTGAGAAATTCATTACGGCTATCAGGAACTTGGGG 1834
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 QY 567 GlnThrProGluPro-----HisTyrGlyTyrGlnGlyHisTrpGlu 580
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 QY 1835 CCAATTGTTGGGGGACAGGGGCTTCTAGCTGCAACCTTCAACTGGACTAAACCTGGC 1894
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 QY 581 AlaThrTrpAlaAspThrSerThrAlaLysSerGlyThrMetThrTrpValThrThrGly 600
 Db |||||:|||||
 QY 1895 TATATTCCTTAATCCAGCGGTATCGGCTCTTAGTCCCTTAATAGCTTATGGAAATGCAATTT 1954
 Db |||||:|||||
 QY 601 TyrAsnProAsnProGluArgAlaSerValProAspSerLeuTrpAlaSerPhe 620
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 QY 1955 ATAGATATTAGCTCTCTCCATTATCTATGAGACTGCAACGAAAGGTTGCGAGGAGAC 2014
 Db |||||:|||||
 QY 621 ThrAspIleArgThrLeuGlnGlnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln 640
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 QY 2015 CGTCTCTTTGGTGTCTCGATTTATCTAATCTCTCCATAAGGATAGTACAAACACCGA 2074
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 QY 641 ArgGlyLeuTrpAlaSerGlyThrAlaAsnPhePheHisLysAspLysSerGlyThrAsn 660
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QY 2846 CGCAATTACAATCTAGACTTAGAGCAAAATACCAATTC 2884
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 ID PM11_CHLPN STANDARD; PRT; 928 AA.
 AC 086164; Q9K299;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable outer membrane protein pmpl1 precursor (Polymorphic membrane
 DE protein 11) (outer membrane protein 4).
 GN PMP11 OR OMP4 OR CPN0449 OR CP0302.
 OS Chlamydia pneumoniae (Chlamydiophila pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiophila pneumoniae.
 NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029/VR-1310;
 RX MEDLINE=99081766; PubMed=9864239;
 RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
 RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
 RT membrane proteins of Chlamydia pneumoniae.";
 RL Infect. Immun. 67:375-383(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity.";
 RL Am. Heart J. 138:S491-S495(1999).
 RN [3]
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 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC
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or send an email to license@sib.ch).

CC EMBL; AJ001311; CAA04672.1; -
 CC EMBL; AJ133034; CAB37072.1; -
 DR EMBL; AB001628; AAD18593.1; -
 DR EMBL; AB002192; AAF38159.1; ALT_INIT.
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 DR PIR; D72077; H86546.
 DR PIR; H86546; H86546.
 DR PHCI-2DPAGE; O86164; -
 DR TIGR; CP0302; -
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145; 2.
 DR TIGRFAMS; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 928 PROBABLE OUTER MEMBRANE PROTEIN PMP11.
 SQ SEQUENCE 928 AA; 98903 MW; 788BCDD62C911402 CRC64;

Alignment Scores:

Pred. No.: 3.49e-104 Length: 928
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 Best Local Similarity: 42.68% Mismatches: 331
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 DB: 1 Gaps: 20

US-09-428-122-1 (1-3000) x PMP11_CHLNP (1-928)

101 ATGAGTCTCTTCCCAAGTTGTATTCTACATTTGCTATTTCCTCTTCCCT- - - - -TTG 154
 1 MetLysThrSerLeuProTprValLeuValSerValLeuAlaPheSerCysHisLeu 20
 155 TCTATGATCTCTACCGAGACAGATTTGGATTCAAGTCGAGTTTCGATGGGAAT- - -AAA 211
 21 GlnSerLeuAlaAsnGluLeuLeuSerProAspSerPheAsnGlyAsnLeuAsp 40
 212 AATGGTAATTTTCAGTCTGTGAGATCGAGAGATGCTGGAACTACCTACCTATTAAAG 271
 41 SerGlyThrPheThrProLysThrSer- - - - -AlaThrThrTyrSerLeuThr 56
 272 GGAATGTCTACTAGAAATATTTCTCGAACAGGCACACATCAACAAAGCTGTTTT 331
 57 GlyAspValPhePheTyrGlu- - - - -ProGlyLysGlyThrProLeuSerAspSerCysPhe 75
 332 AACAACTAAGGCGGATTTGACTTTCACAGGTAACGGGAACCTCTATTGTTCCAAACG 391
 76 LysGlnThrThrAspAsnLeuThrPheLeuGlyAsnGlyHisSerLeuThrPheGlyPhe 95
 392 GTGGATCGAGGACTGTAGAGGCGCTGTGTTAAACAGAGCGGTGGTAGATAATCTACC 451
 96 IleAspAlaGlyThrHisAlaGlyAlaAla- - - - -SerThrThrAlaAsnLysAsnLeu 114
 452 ACGTTTATAGGTTTCTTCGCTATCTTTATTTCGCTCTCTGGAAGTTCGATAACTACC 511
 115 ThrPheSerGlyPheSerLeuLeuSerPheAspSerProSerThrThrValThrThr 134
 512 GCGAAAGGAGCGGTAGCTGTCTACCGGTAGCTTTGAGTTTGACAAATAATGTCAGTTTG 571
 135 GlyGlnGlyThrLeuSer- - - - -SerAlaGlyGlyValAsnLeuGluAsnLeuAryGlyLeu 153
 572 CTCTTCAGCAAAACTTTTCAACCGATAATGGCGGTGCTATACCGCAAAACTCTTTTCA 631
 154 ValValAlaGlyAsnPheSerThrAlaAspGlyGlyAlaIleLysGlyAlaSerPheLeu 173
 632 TTAACAGGACTACAATGTCTGCTCTGTTCTGAAATACCTCTCAAGAAAGCGGA 691
 174 LeuThrGlyThrSerGlyAspAlaLeuPheSerAsnAsnSerSerSerThrLysGlyGly 193
 692 GCCATTGAGACTTCCGATGCGCTTACCATTACTGGAAACCAAGGGGAGTCTCTTTTCT 751
 194 AlaIleAlaThrThrAlaGlyAlaAlaArgIleAlaAsnAsnThrGlyTyrValArgPheLeu 213

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 812 AATAATGCTAAAGTTTCTTTTATTGACATAAGGTCACAGGAGCGAGCTCTCAACAACG 871
 234 AsnAsnLysPheLeuTyrPhe- - - - -GluGlyAsnAlaIleLysThrThr 248
 872 GGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAGGTCCAC 931
 249 - - - - -GlyGlyAlaIleCysAsnThrLysAlaSerGlySerProGluLeuIle 264
 932 CTCACCTGGAATCAGATGTTACTCTTCACCAACAATATCATCACAACACGGGAGAGCT 991
 265 IleSerAsnAsnLysThrLeuIlePheAlaSerAsnValAlaGluThrSerGlyGlyAla 284
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 442 LysGlyValThrLeuGluSerThrSerPheSerGlnGluAlaGlySerLeuLeuGlyMet 461
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 462 AspSerGlyThrThrLeuSerThrThrAlaGlySerIleThrIleThrAsnLeuGlyIle 481
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 1703 CATAGTTTAAAGAACTCCTCAGTCTCAGCATCTTAGCATCAAAAGCTTCGGAACGTA 1762
 522 HisMetPheSerHisAspGlnLeuPheSerLeuLeuIleThrValAspAlaAspVal 541
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 542 AspThrAsnValAspIleSerSerLeuIleProValProAlaGluAspProAsnSerGlu 561
 1811 TACGGCTATCAGGGAACCTTGGGGCCCAATTGTTGGGGACAGGGCTTCTACGACT- - - 1867

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Db      562  TyrGlyPheGlnGlyGlnTrpAsn---ValaenTrpThrThrAspThrAlaThrAsnThr 580
QY      1868  -----GCAACCTTCACTGGCTAAACTGGCTATATCTCTAAATCCGAGCGTATCGGC 1921
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QY      1922  TCTTTAGTCCCTAAATAGCTTATGGAATGCATTTATAGATATTATAGCTCTCTCCATATCTT 1981
Db      601  AlaLeuValCysAsnThrLeuTrpGlyValPheThrAspIleArgSerLeuGlnGlnLeu 620
QY      1982  ATGGAGACTGCCAAACGAAGGTTGCAGGAGACCGTCTTTTGTGTGCTGCTGATATCT 2041
Db      621  ValGluIleGlyAlaThrGlyMetGluHisLysGlnGlyPheTrpValSerSerMetThr 640
QY      2042  AACTTTCTTCATAAGATAGTACAAAACACACGCGGTTTCGCCATTTGAGTGGCGGT 2101
Db      641  AsnPheLeuHisLysThrGlyAspGluAsnArgLysGlyPheArgHisThrSerGlyGly 660
QY      2102  TATGTCATAGGAGAAACCTACATCTTGTTCAGATAAGATCTTAGTGTCTCATTTGT 2161
Db      661  TyrValIleGlyGlySerAlaHisThrProLysAspAspLeuPheThrPheAlaPheCys 680
QY      2162  CAGCTCTTTGGAGAGATAGAGACTCTTTGTAGTAAAGATCAAGGTACAGTCTACGGA 2221
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QY      2222  GGAACCTCTATTACACGACACAAACAC-----TATATCTCTCTT--- 2263
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QY      2264  CCTTGCAAACTACGCGCTTGTTCGTGTCTTATGTTCTCTACAGATTCCTGTTCTCTT 2323
Db      721  ArgAlaLysPheSerGluSerAlaIleGluLysPheProArgGluIleProLeuAlaLeu 740
QY      2324  TCAGAAACCTTAGTACACCATACGGATACGATCTGAAACCAAGTATACACATAT 2383
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QY      2384  CCTACTGTTAAGAGNAGCTGGGGNATGATAGTTTCGCTTTAGATTCGGTGGAGAGCT 2443
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Db      781  ProPheValLeuSerAsnProHisProLeuPheLysThrPheIleProGlnMetLysVal 800
QY      2501  CAGTTTGTCTATGCACATCAGAAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTT 2560
Db      801  GluMetValTyValSerGlnAsnSerPhePheGluSerSerSerAspGlyArgGlyPhe 820
QY      2561  GGAAGTACCGCTCTGTGTAATCTTCCTTACTATCGGATCCGATTTGATGAAGGAATCA 2620
Db      821  SerIleGlyArgLeuLeuAsnLeuSerIleProValGlyAlaLysPhe---ValGlnGly 839
QY      2621  GACTGCCAAGATGCA---ACGTACAATCTAACTCTGTGTTACTGTGATCTTGTTCGT 2677
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QY      2678  AGTAACCCGACTGTACGACACACTGCGAATAGCGGTGATCTTGTGAAACCTTCGGT 2737
Db      860  AsnAsnProGlnSerThrAlaThrLeuValMetSerProAspSerTrpLysIleArgGly 879
QY      2738  ACGAATTTGGCAGACAGCTTTAGTCTCTGTGTCGAGGGAACCATTTTGTCTTAATCA 2797
Db      880  GlyAsnLeuSerArgGlnAlaPheLeuLeuArgGlySerAsnAsnTyValTyAsnSer 899
QY      2798  AATTGTAAGCTTTAGCCAAATTTCTTTTGAATTGCGTGGGTCTATCGCAATTAACAT 2857
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QY      2858  GTAGACTTAGGACCAAAATACCAATTC 2884

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Db      920  ValaaspValGlyThrLysLeuArgPhe 928
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AC Q9Z3A1; Q9RB73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp2 precursor (Polymorphic membrane
protein 2) (Outer membrane protein 7).
GN PMP2 OR OMP7 OR CPN0013 OR CP0761.
OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_Taxid=83558;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=105139856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Lihner K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae A839.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
(POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 673.
-----
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EMBL; AJ133035; CAB37083.1; -
EMBL; AE001586; AAD18172.1; -
EMBL; AF002235; AAF38561.1; -
EMBL; AF002545; BAA98223.1; ALT_FRAME.
PIR; E72130; E72130.
PHCI-2DPAGE; Q9Z3A1; -.

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Db      524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArg 543
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QY      2081 TTTCCGCAATTTGAGTGGCGGTATGTCTATGATAGGAGAACCTACATACATCTTTCAGATAAG 2140
Db      564 PheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp 583
QY      2141 ATCTCTAGTCTGCATTTTGTCTAGCTCTTGTGGAAGATAGAGACTACTTTGTAGCTAAG 2200
Db      584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThr 603
QY      2201 AATCAAGGTACAGTCTACGGAGAACTCTCTATTACCGACACACGAAACCTATATCTCT 2260
Db      604 AsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSer 623
QY      2261 CTTCTCTGTC-----AAACTACCGCCTTGTCTGTCTTATCTTCTTCTCT 2302
Db      624 ValValSerIleLeuLeuGlyGluGlyLeuArgGluIleLeuLeuProTyrValSer 643
QY      2303 ACAGAGATTCCTGTTCTCTTTTCAGAAACCTTACCTACCCATACGGAATAACGATCTG 2362
Db      644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
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QY      2408 AATGATGATTTTGGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTAGATGAAGTCT 2467
Db      684 GlyTyrValTyrAlaGlyGluLeuGlyThrArg-----ValAlaValGluAsnThrSer 701
QY      2468 -----CTATTGACAGTACATGCGCTTCATGAATTCGATTTGCTTATGACAT 2518
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QY      2519 CAGGAAGGTTTAAAGACAGGACAGACAGCTCGTGAATTTGGAGTAGCGCTCTGTG 2578
Db      722 GlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
QY      2579 AATCTTGCTTACCTTACCGATCCGATTCGATTTGATAGGAATCAGACTGCCAAGATGCAACG 2638
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QY      2639 TACAATCTAACTCTGGTTACTGTGATCTGTGATCTGTGATTAACCCGACTGTACGACA 2698
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QY      2699 ACATCTCGAATTAGCGGTGATTCTTGGAAACCTTCGGTACGATTTTGGCAAGACAGCT 2758
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QY      2759 TTAGTCTCTGTCGAGGAACCATTTTGTCTTTTAACTCAATTTTGAAGCCCTTAGCCAA 2818
Db      800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsn 819
QY      2819 TTTTCTTTTGAATTCGGTGGTCTATCTCGCAATTAATGATAGACTTAGGAGCAAAATAC 2878
Db      820 PheGlyPheGluTyrPargGlySerSerArgSerTyrAsnValAspAlaGlySerLysIle 839
QY      2879 CAATTC 2884
Db      840 LysPhe 841

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RESULT 7

PMP6_CHLPN

ID -PMP6_CHLPN STANDARD; PRT; 1276 AA.

AC Q92899; OSJRW2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE      Probable outer membrane protein pmp6 precursor (Polymorphic membrane
GN      protein 6).
DN      PMP6 OR CEN0444 OR CP0309.
OS      Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC      Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX      NCBI TaxID=83558;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CNL029;
RX      MEDLINE=9920606; PubMed=10192388;
RA      Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RT      Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT      "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL      Nat. Genet. 21:385-389(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AR39;
RX      MEDLINE=20150255; PubMed=10684935;
RA      Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RT      White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RT      Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RT      Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RT      Eisen J., Fraser C.M.;
RT      "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL      pneumoniae AR39.";
RL      Nucleic Acids Res. 28:1397-1406(2000).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=J138;
RX      MEDLINE=20330349; PubMed=10871362;
RA      Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RT      Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT      "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT      from Japan and CWL029 from USA.";
RL      Nucleic Acids Res. 28:2311-2314(2000).
CC      -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC      (POTENTIAL).
CC      -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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CC      or send an email to license@sib-sib.ch).
DR      EMBL; AE001627; AAD18588.1; -
DR      EMBL; AE002193; AAF38166.1; -
DR      EMBL; AP002546; BAA98652.1; -
DR      PIR; B72078; B72078.
DR      PIR; B86546; B86546.
DR      PIR; C81591; C81591.
DR      PHCI-2DPAGE; Q92899; -
DR      TIGR; CP0309; -
DR      InterPro; IPR006315; Autotransport.
DR      InterPro; IPR003368; Chlamydia_PMP.
DR      Pfam; PF02415; DUF145; 2.
DR      TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR      TIGRFAMs; TIGR01376; POMP repeat; 14.
KW      Outer membrane; Signal; Multigene family; Complete proteome.
FT      SIGNAL 1 23 POTENTIAL.
FT      CHAIN 24 1276 PROBABLE OUTER MEMBRANE PROTEIN PMP6.
FT      CONFLICT 421 421 E -> ECGGAILAFIDSGVSDKTGLSIANNQEVSLTNSA
FT      ATVSGGAIYATKCTLTGNGSLTGDNGTAGTSGGAIYETED
FT      FTLTGTGTFTFTNTAKTGTALYSKGNNSISGNTLLPSC
FT      NKATGPSNSANOE (IN REF. 1).
SQ      SEQUENCE 1276 AA; 132127 MW; C97FA0662C88E0B CRC64;
Alignment Scores: 1.82e-79 Length: 1276
Pred. No.: 1444.00 Matches: 382
Score: 41.62% Conservative: 157
Percent Similarity:

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Best Local Similarity: 29.50% Mismatches: 370
Query Match: 26.70% Indels: 386
DB: 1 Gaps: 26
US-09-428-122-1 (1-3000) x PMP6_CHLPN (1-1276)

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QY 218 AAT-----TTTTACGTTCTGTAGCTCAGGAGATGCTGGAACCTACCTACCTATTAAAG 271
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QY 787 -----787
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QY 788 -----ACAGAGCCTCGGTGACTATTCTTAATATGCTAAA 823
Db 253 AlaLysThrGlyGlyAlaTrpSerSerAspAsnLeuAlaLeuThrGlyAsnThrGln 272
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Db 353 ThrAlaGlyCysGlyGlyAlaIleTyrThrGluThrGluAspPheSerLeuLysGlySer 372
QY 976 -----976
Db 373 ThrGlyThrValThrPheSerThrAsnThrAlaLysThrGlyGlyAlaLeuTyrSerLys 392
QY 976 -----976
Db 393 GlyAsnSerSerLeuThrGlyAsnThrAsnLeuLeuPheSerGlyAsnLysAlaThrGly 412
QY 976 -----976
Db 413 ProSerAsnSerSerAlaAsnGlnGluGlyCysGlyGlyAlaIleLeuSerPheLeuGlu 432
QY 976 -----976
Db 433 SerAlaSerValSerThrLysLysGlyLeuTrpIleGluAspAsnGluAsnValSerLeu 452
QY 976 -----976
Db 453 SerGlyAsnThrAlaThrValSerGlyGlyAlaIleTyrAlaThrLysCysAlaLeuHis 472
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QY 976 -----976
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QY 976 -----976
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QY 1028 CTTACCTTATTCAGTAGAATAAGTAGTCTCAATGGAGGTACAGCTCTCAAGGTGGAGCCATA 1087
Db 633 ProValSerPheThrAsnAsnSer-----GlyGly-----LysGlyGlyAlaIle 647
QY 1088 GCTATCGAAGATAGTGGGAATTGAGTTTATCCCGGATAGTGTGATGATGCTCTTTT 1147
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QY 1148 GGAATATACAGTCACTTCTACTACTCTCTGGACGAATAGAGTAGTAGTCTAGTACGACG 1207
Db 668 GlyAsnArgAlaThrGluGlyThrSerThrProAsn-----SerIleHisLeuGlyAla 685
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RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA".
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -/- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC -/- (POTENTIAL).
 CC -/- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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 CC
 DR ENBL; AJ133035; CAB37075.1; -
 DR ENBL; AE001585; AAD18163.1; -
 DR ENBL; AE002237; AAF38570.1; -
 DR ENBL; AP002545; BAA98215.1; -
 DR PIR; B72131; B72131.
 DR PIR; E86491; E86491.
 DR TIGR; CP0770; -
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145; 1.
 DR TIGRFAMS; TIGR01376; POMP repeat; 5.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 922 PROBABLE OUTER MEMBRANE PROTEIN PMP1.
 FT CONFLICT 14 14 F -> L (IN REF. 1).
 FT CONFLICT 375 375 Y -> C (IN REF. 1).
 FT CONFLICT 606 606 D -> N (IN REF. 1).
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 Score: 1442.50 Matches: 351
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 QY 170 GAGACAGTTTGGATTCAAGTCGCGAGTTTCGATGGGAATAAAATGTAATTTTCAGTT 229
 DB 28 ThrIleSerLeuThrProGluAspSerPheHisGlyAspSerGlnAsn-----AlaGlu 45

QY 230 CGTGAGAGTCAGAGAGATCTCGGAACCTACCTACCTATTATTAAGGGAATAATCTCACTCTAGAA 289
 DB 46 ArgSerTyrAsnValGlnAlaGlyAspValTyrSerLeuThrGlyAspValSerIleSer 65
 QY 290 AATATTCTCGGAACAGGACAGCAATACAAAAAGCTGTTTAAACAACTTAAGGGCGAT 349
 DB 66 AsnVal-----AspAsnSerAlaLeuAsnLysAlaCysPheAsnValThrSerGlySer 83
 QY 350 TTGACTTTCCAGGTAAACGGGAACCTCTATTGTTCCAAACGGTGGATCAGGAGCTGTA 409
 DB 84 ValThrPheAlaGlyAsnHisGlyLeuTyrPheAsnAsnIleSerSerGlyThrThr 103
 QY 410 GCAGGGCTGCTGTTAACAGCAGCGTGGTAGATAAATCTACCACG---TTTATAGGGTTT 466
 DB 104 LysGluGlyAlaValLeuCysCysGlnAspProGlnAlaThrAlaArgPheSerGlyPhe 123
 QY 467 TCTTCGTATCTTTTATTGCGTCTCTGGAAGTTCGATAACTACCGGCAAGAGCGGTT 526
 DB 124 SerThrLeuSerPheIleGlnSerProGlyAspIleLysGluGlnGly----- 139
 QY 527 AGCTGC-----TCTACGGGTAGCTTGTAGTTTGTACAAAAAATGTCTGCTTCTTCAGC 580
 DB 140 ---CysLeuTyrSerLysAsnAlaLeuMetLeuLeuAsnAsnTyrValValArgPheGlu 158
 QY 581 AAAAAGTTTCAACGGATAATGCGGTGCTATCACCGCAAAACCTCTTTCATTACAGGG 640
 DB 159 GlnAsnGlnSerLysThrLysGlyGlyAlaIleSerGlyAlaAsnValThrIleValGly 178
 QY 641 ACTACAATCTCAGCTCTGTTTCTGAAATACTCTCTCAAGAAAGGCGGAGCCATTTCAG 700
 DB 179 AsnTyrAspSerValSerPheTyrGlnAsnAlaAlaThr---PheGlyAlaIleHis 197
 QY 701 ACTTCGATGCCCTTACCATTACTGAAACCAAGGGGAAGTCTCTTTTCTGACATACT 760
 DB 198 SerSerGlyProLeuGlnIleAlaValAsnGlnAlaGluIleArgPheAlaGlnAsnThr 217
 QY 761 TCTTCGGAT---TCTGGAGCTGCAATTTTACAGAAGCCTCGTGACTATTCTTAATAT 817
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 QY 818 GCTAAAGTTTCTTTTATTGACAATAAGTTCACAGGAGGAGCTCTCTCAACACGGGGAT 877
 DB 238 AlaTyrValLeuPheArgGluAsnGlu-----AlaLeuThrThrAlaIle 252
 QY 878 ATGTACAGGAGTCTATCTGTCTTATAAAACCTAGTACAGATACTAAG----- 925
 DB 253 GlyLysGlyGlyAlaValCysCysLeuProThrSerGlySerThrProValProIle 272
 QY 926 GTCACCTCAGTGGAAATCAGATGTTACTTCTTCAGCAACAATACATACGACACGCGGA 985
 DB 273 ValThrPheSerAspAsnLysGlnLeuValPheGluArgAsnHisSerIleMetGlyGly 292
 QY 986 GGAGCTATCTATGTGAAAGCTCGAACTGGCTCCGAGGAGCTTACCCCTATTTCAGTAGA 1045
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 QY 1226 TTGCGTTTCGCTCGGTAGAGCCATCTACTTCTATGATCCCATCACTACAGATCATCC 1285
 DB 369 LeuGlnAlaArgAsnGlyTyrSerIleGluPheTyrAspProIleThr-----SerGlu 386
 QY 1286 ACACAGTTTACAGATGCTTTAAAGTTAATGAGATCCCGGAGATTCCTGCATCATATAT 1345

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Db      387 AlaAspGlySerThrGlnLeuAsnIleAsnGlyAspProLysAsnLys-----GluTyr 404
QY      1346 ACAGGAAACATCATCTTCACAGGAGAAAGATTATCAGACAGACAGCGCGAGATTCTAAA 1405
Db      405 ThrGlyThrIleLeuPheSerGlyGluLys-----SerLeuAlaAsnAspProArg 421
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QY      1466 CATGAGAGTCTCTCAGACTCAGCATTCTCAACAGCGAGATTCTCGTCTCGAAATG 1525
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QY      1526 GACGTAGAACTACTCTA---GAACCTGCTGATACATACATCAAAATTTGGTCAAT 1582
Db      462 AspLeuGlyThrLysLeuIleAlaSerLysGluAspIleAlaIleThrGlyLeuAlaIle 481
QY      1583 AACATCAGTCTTATAGACGGTGCAGAGGCAAGGCAAAA---ATAGAAACCAAGAGCTACGTCA 1639
Db      482 AspIleAspSerLeuSerSerSerThrAlaAlaValIleLysAlaAsnThrAlaAsn 501
QY      1640 AAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCGCAGCGCACGTTTATGAA 1699
Db      502 LysGlnIleSerValThrAspSerIleGluLeuIleSerProThrGlyAlaAlaTyrGlu 521
QY      1700 AATCATAGTTTAAAGAAATCTCAGTCCTCAGACATCTTTAGAGCTCAAA-----GCTTCT 1753
Db      522 AspLeuArgMetArgAsnSerGlnThrPheProLeuLeuSerLeuGluProGlyAlaGly 541
QY      1754 GGAAGTCTTAAAGACAGCAGCGCA-----GTGATCTCCAGATCTTAAATGGGT 1798
Db      542 GlySerValThrValThrAlaGlyAspPheLeuProValSerPro----- 556
QY      1799 GAGAAATTCATATAGCGTATCAGGCACTTGGGGCCCAATTTGTTGG---GGACAGGG 1855
Db      557 -----HisTyrGlyPheGlnGlyAsnTrp---LysLeuAlaTrpThrGlyThrGly 572
QY      1856 GCTTCTACGACTGCAACCTTCAACTGGAGTAAACTGGCTATATCTTAATCCCGAGCGT 1915
Db      573 ---AsnLysValGlyGluPhePheTrpAspLysIleAsnTyrLysProArgProGluLys 591
QY      1916 ATCGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTAAGATATAGTCTCTCTCCAT 1975
Db      592 GluGlyAsnLeuValProAsnIleLeuTrpGlyAsnAlaValAspValArgSerLeuMet 611
QY      1976 TATCTTATGGAGACTGCAACGAGGGTTCAGGAGACCGTCTTTTGGTGTGCTGGA 2035
Db      612 GlnValGlnGluThrHisAlaSerSerLeuGlnThrAspArgGlyLeuTrpIleAspGly 631
QY      2036 TTAICTAACTCTTCCATPAAGATAGTACAAAACACAGCAGCGGTTTCGCCATTTGAGT 2095
Db      632 IleGlyAsnPhePheHisValSerAlaSerGluAspAsnIleArgTyrArgHisAsnSer 651
QY      2096 GCGGTATATCTCATAGGAGAACTCATACTTGTTCAGATAGACTTCTTAGTGTGCTGCA 2155
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QY      2156 TTTTGTGAGCTCTTTGGAAGAGATAGAGACTTCTTTGTAGCTTAAGATCAAGGTACAGTC 2215
Db      672 PheSerGlnLeuPheSerArgAspLysAspTyrAlaValSerAsnGluLysTyrArgMet 691
QY      2216 TACGAGGAAGTCTCTTATACAGCAACACGAAAC-----TATATC 2257
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QY      2315 GTTCTCTTTTTCAGGAACCTTAGCTACACCCATAGGATACAGTCTGAAACACAGTAT 2374

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Db      732 MetIlePheHisPheLeuCysAlaTyrGlyHisAlaThrAsnAspMetLysThrAspTyr 751
QY      2375 ACAACATATCTCTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTTAAAGATTCGGT 2434
Db      752 AlaAsnPheProMetValLysAsnSerTrpArgAsnAsnCysTrpAlaIleGluCysGly 771
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QY      2552 CGTGAATTTGGAAGTAGCCGCTTTGTGAATCTTCCTATCCCTATCCGATCCGATTTGAT 2611
Db      812 ArgArgPheSerAsnGlySerLeuThrSerIleSerValProLeuGlyIleArgPheGlu 831
QY      2612 AAGGAATCAGACTCCCGAGATGCAACGCTACATCTAATCTCTGTTGTTATCTGTGTGATCTT 2671
Db      832 LysLeuAlaLeuSerGlnAspValLeuTyrAspPheSerPheSerTyrIleProAspIle 851
QY      2672 GTTCGTAGTAAACCCGACTGTACGACACACTGCGAATTAGCGGTGATCTTGGAAAC 2731
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QY      2792 AACTCAATTTTGAAGCTTTAGCCAAATTTCTTTGAATTCGCTGGGTCTATCTCGCAAT 2851
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QY      2852 TACAATGTAGACTTAGGAGCAAAATACCAATTC 2884
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RESULT 9
PM13 CHLPN
ID PM13 CHLPN STANDARD; PRT; 973 AA.
AC Q92856; Q9K2A1; Q9Z4I0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Probable outer membrane protein pmp13 precursor (Polymorphic membrane protein 13) (Outer membrane protein 14).
GN PMP13 OR OMP14 OR CPN0453 OR CP0299.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
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RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CML029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314 (2000).
 RN [4]
 RP SEQUENCE OF 1-262 FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madсен A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity.";
 RL Am. Heart J. 138:S491-S495(1999).
 CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC -!- (POTENTIAL)
 CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC
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 CC
 DR EMBL; AB001629; RAD18595.1; -;
 DR EMBL; AB002191; RAF38156.1; ALT_INIT.
 DR EMBL; AP002546; ERA98660.1; -;
 DR EMBL; AJ133034; CAB37074.1; -;
 DR PIR; B86547; B86547.
 DR PIR; F72076; F72076.
 DR PHCI-2DPAGE; 09Z896; -;
 DR TIGR; CP0299; -;
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; DUF145; 3.
 DR TIGRPFAM; TIGR01376; POMP repeat; 7.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 973 PROBABLE OUTER MEMBRANE PROTEIN PMP13.
 FT CONFLICT 258 258 N -> Y (IN REF. 4).
 SQ SEQUENCE 973 AA; 102761 MW; E02A69F611DBEF2 CRC64;

Alignment Scores:
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 Score: 1377.50 Matches: 350
 Percent Similarity: 49.95% Conservative: 153
 Best Local Similarity: 34.76% Mismatches: 391
 Query Match: 25.47% Indels: 113
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US-09-428-122-1 (1-3000) x PMP13_CHLPN (1-973)

QY 326 TGTTTTAAACACACTAAGGCGGATTTGACATTTCACAGGTAACGGGAACCTCTATTGTTTC 385
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 77 CysPheSerAsnArgAlaGlyAlaLeuGlnLeuGlyLysGlyValPheSerPhe 96
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 386 CAACACGGTGGATGACGGGACTGTAGCAGGGGCTCTGTAAACAGCAGCGGTGTAGATAAA 445
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 97 LeuAsnle---ArgSerSerAlaAspGlyAlaAlaIleSerSerValIleThrGluAsn 115
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 446 -----TCTACCAGTTTATAGGGTTTCTTCGGCTATCTTTT----- 481
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 QY 116 ProGluLeuCysProLeuSerPheSerGlyPheSerGlnMetIlePheAsnAsnCysGlu 135
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 482 -----ATTGCGTCTCTGGAGTTTCGATACTACCGCAAGAGCGGTGTAGCTGC 532
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 136 SerLeuThrSerAspThrSerAlaSerAsnValIleProHisAlaSerAlaIleThrAla 155
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 533 TCTACGGGTAGCTGAGTTTGCACAAAATGTCAGTTTGTCTTTCAGCAAAAACCTTTTCA 592
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 156 ThrThrProMetLeu---PheThrAsnAsnAspSerIleLeuPheGlnTyrAsnArgSer 174
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 QY 593 ACGGATATGCGGTGTATTCACCGCAAAAACCTTTCATTAACAGGACTACATGTCA 652
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 175 AlaGlyPheGlyAlaAlaIleArgGlyThrSerIleThrIleGluAsnThrLysLysSer 194
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 653 GCTCTGTTTCTGAAATACCTCTCAAGAAAGCGGAGCCATTACAGACTTCGATGCC 712
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 195 LeuLeuPheAsnGlyAsnGlySerIleSerAsnGlyAlaIleThrGlySerAlaAla 214
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 713 CTTACCAATTACTGAAACCAAGGGGAAGTCTCTTTTCTTGAC----- 754
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 215 IleAsnLeuIleAsnAsnSerAlaProValIlePheSerThrAsnAlaThrGlyIleTyr 234
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 754 ----- 754
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 235 GlyGlyAlaIleTyrLeuThrGlyGlySerMetLeuThrSerGlyAsnLeuSerGlyVal 254
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 755 -----AATACTTCTTCGGATTCTCGAGCTGCAATTTTACAGAAGCCTCGGTGACT 805
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 255 LeuPheValAsnAsnSerArgSerGlyAlaIleTyrAlaAsnGlyAsnValThr 274
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 806 ATTTCTAATAATGCTTAAAGTTTCTCTTTTATGACATAAGGTCACAGAGCAGAGTCC--- 862
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 275 PheSerAsnAsnSerAspLeuThrPheGlnAsnAsnThrAlaSerProGlnAsnSerLeu 294
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 863 -----TCAACACAGGGGGATATGTCA---CGAGGT 889
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 295 ProAlaProThrProProThrProAlaValThrProLeuLeuGlyTyrGlyGly 314
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 890 GCTATC---TGT-----GCTTATAAACTAGTACAGATACTAAGGTCAACCTCACT 937
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 315 AlaIlePheCysThrProProAlaThrProProThrGlyValSerLeuThrIleSer 334
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 938 GGAAATCAGATGTTACTTTCAGCAACAATACATCAGCAACAGCGGAGGAGCTATCTAT 997
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 335 GlyGluAsnSerValThrPheLeuGluAsnIleAlaSerGluGlnGlyGlyAlaLeuTyr 354
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 998 GTGAAAAGCTCGAAGTCTCCGAGAGCTTACCTTCTCAGTAGAAAATAGTCTCAT 1057
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 355 GlyLysLysIleSerIleAspSerAsnLysSerThrIlePheLeu----- 369
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1058 GGAGGTACAGCTCTTAAAGTGGAGCCATAGTATCGAAGATAGTGGGAATTTAGATTTA 1117
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 370 GlyAsnThrAlaGlyLysGlyAlaIleAlaIleProGluSerGlyGluLeuSerLeu 389
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1118 TCCGCCGATAGTGTGACATTGCTTTTATAGGGAAT---ACAGTCACCTTACTACTCT 1174
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 390 SerAlaAsnGlnGlyAspIleLeuPheAsnLysAsnLeuSerIleThrSerGlyThrPro 409
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1175 GGGACGAATAGAAATGATGATTCAGTATGGAACAGTGCAGAAATGACAGCTTTGGCTCT 1234
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 410 -----ThrArgAsnSerIleHisPheGlyLysAspAlaLysPheAlaThrLeuGlyAla 427
 Db |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1235 GCTGCTGGTAGAGCCATCTACTTCTATGATCCATACTACAGGA-----TCATCCCA 1288

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Db      428 ThrGlnGlyThrLeuThrPheThrAspProIleThrSerAspLeuSerAlaAla 447
QY      1289 ACAGTTACAGATCTTAAAGTAAAT---GAGACTCCGGCAGATTCGTCACTACAAAT 1345
Db      448 SerAlaAlaThrValValValAsnProLysAlaSerAlaAspGlyAla-----Tyr 465
QY      1346 ACAGGGACATCATCTTCACAGGAGAAAGTTATCAGACAGAGCCGACAGTTCTAAA 1405
Db      466 SerGlyThrIleValPheSerGlyGluThrLeuThrAlaThrGluAlaAlaThrProAla 485
QY      1406 AATCTTACTTCAAGCTACTACAGCTGTAACCTCTTTCAGGAGGTACTCTACTCTTAAAA 1465
Db      486 AsnAlaThrSerThrLeuAsnGlnLysLeuGluGluGlyGlyThrLeuAlaLeuArg 505
QY      1466 CATGAGTACTCTCAGACTCAGGCATTCATCAACAGGCAGATTCCTCGTTCGAAATG 1525
Db      506 AsnGlyAlaThrLeuAsnValHisAsnPheThrGlnAspGluLysSerValValIleMet 525
QY      1526 GACGTAGGAACACTCTAGAACCTGCTGATACG-----ACC 1564
Db      526 AspAlaGlyThrThrLeuAlaThrThrAsnGlyAlaAsnThrAspGlyAlaIleThr 545
QY      1565 ATAAACAATTTGGTCATTAAACATCATGTTCTATAGACGGTGCAGAAAGCAAAATAGAA 1624
Db      546 LeuAsnLysLeuValIleAsnLeuAspSerLeuAspGlyThrLysAlaAlaValValAsn 565
QY      1625 ACCAAGACTACTCAAAAATCTGATTTATCTGAACCATCATCTTATTGACCCGACG 1684
Db      566 ValGlnSerThrAsnGlyAlaLeuThrIleSerGlyThrLeuGlyLeuValLysAsnSer 585
QY      1685 GCACGTTTATGAAATCATAGTTTAAGAAATCCT-----CAGTCCTACGACATCTTA 1738
Db      586 GlnAspCysCysAspAsnHisGlyMetPheAsnLysAspLeuGlnGlnValProIleLeu 605
QY      1739 GAGCTCAAGACT---TCTGGAACTGTAAACAAGCAGCGAGTCAGATCCAGATCCTATAATG 1795
Db      606 GluLeuLysAlaThrSerAsnThrValThrThrAspPheSerLeuGlyThrAsnGly 625
QY      1796 GGTGAGAAATCCATTACGGCTATCAGGGAATCTGGGGCCCAATTTGTTGGGGACAGG 1855
Db      626 TyrGlnGlnSerProGlyThrGlyThrGlnGlyThrTrpGluPheThrIleAspThrThr--- 644
QY      1856 GCTTCTACGACGCACTTCACTGACTAAATCGGTAAATCGGTATATTCCTAATCCGAGCT 1915
Db      645 ---ThrHisThrValThrGlyAsnTrpLysLysThrGlyThrLeuProHisProGluArg 663
QY      1916 ATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTCTCCAT 1975
Db      664 LeuAlaProLeuIleProAsnSerLeuTrpAlaAsnValIleAspLeuArgAlaValSer 683
QY      1976 TATCTTATGGAGACTGCAAACGAAGGTGTCAGGAGACCGCTGCTTTTGGTGGCTGA 2035
Db      684 GlnAlaSerAlaAlaAspGlyGluAspValProGly---LysGlnLeuSerIleThrGly 702
QY      2036 TTATCTAATCTTCCATAAGATAGTAGTACAAAACACGACGCGGGTTTCGCCATTTGACT 2095
Db      703 IleThrAsnPhePheHisAlaAsnHisThrGlyAspAlaArgSerThrArgHisMetGly 722
QY      2096 GCGGCTTATGTCATAGGAGGAAACCTACATCTTGTTCAGATAAGATCTTATAGTGTGCA 2155
Db      723 GlyGlyThrLeuIleAsnThrThrArgIleThrProAspAlaAlaLeuSerLeuGly 742
QY      2156 TTTTGTACGCTTTTGGAGAGATAGACTACTCTTTGTAGCTTAAGATCAAGGTACAGTC 2215
Db      743 PheGlyGlnLeuPheThrLysSerLysAspThrLeuValGlyHisGlyHisSerAsnVal 762
QY      2216 TACGAGGAGACTCTATTACAGCACACGAAACCTATATCTCTCTCTCTCTGCAACTA 2275
Db      763 TyrPheAlaThrValThrSerAsnIleThrLysSerLeuPheGly----- 777
QY      2276 CGGCGCTTGTGCTGCTTATGTTCTCTACAGAGATTCCTGTTCTCTTTTCAGAAACCTT 2335

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Db      778 -----SerSerArgPhePheSerGlyThr 786
QY      2336 AGC-----TACACCATACGATTAACATCTGAAACCAAGATATACACATATCT 2386
Db      787 SerArgValThrThrSerArgSerAsnGluLysValLysThrSerThrLysLeuPro 806
QY      2387 ACTGTTAAAGAGCTGGGGAATCATAGTTTCGCTTTAGATTCGGTGGAGAGCTCG 2446
Db      807 LysGlyArgCysSerTrpSerAsnAsnCysTrpLeuGlyGluLeuGluGlyAsnLeuPro 826
QY      2447 ATTTCTTAGATGAAAGTGCTCTA---TTTGACAGTACATGATCCCTTCATGAAATTCGAG 2503
Db      827 IleThrLeuSerSerArgIleLeuAsnLeuLysGlnIleProPheValLysAlaGlu 846
QY      2504 TTTGCTATGACATCAGAAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTCGA 2563
Db      847 ValAlaThrAlaThrHisGlyGlyIleGlnGluAsnThrProGluGlyArgIlePheGly 866
QY      2564 AGTAGCCGCTTGTGAATCTTCCCTTACCTCGGATCCGATTTGATAGGAATCAGAC 2623
Db      867 HisGlyHisLeuLeuAsnValAlaValProValGlyValArgPheGlyLysAsnSerHis 886
QY      2624 TGCCAAGATGCAACGTCACAATCTACTCTTGGTTTACTGTGATCTTGTCTAGTAAAC 2683
Db      887 AsnArgProAspPheThrThrIleValAlaThrAlaProAspValThrArgHisAsn 906
QY      2684 CCGGCTCTACGACAACTCGAATAGCGGTGATTTCTTGAAACCTTCGGTACGAAT 2743
Db      907 ProAspCysAspThrThrLeuProIleAsnGlyAlaThrTrpThrSerIleGlyAsnAsn 926
QY      2744 TTGGCAACACAAAGCTTTAGTCTCTCGTCGCGGACCACTTTTGTCTTAACTCAATTTT 2803
Db      927 LeuThrArgSerThrLeuLeuValGlnAlaSerSerHisThrSerValAsnAspValLeu 946
QY      2804 GAAGCTTTAGCCAAATTTCTTTGATTTGGTGGGTCTATCTCGCAATTAACAATCTAGAC 2863
Db      947 GluIlePheGlyHisCysGlyCysAspIleArgThrSerArgGlnThrThrLeuAsp 966
QY      2864 TTAGAGCAAAATACCAATTC 2884
Db      967 IleGlySerLysLeuArgPhe 973

RESULT 10
PMPG_CHLTR
ID PMPG_CHLTR STANDARD; PRT; 1013 AA.
AC 084879;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmpG precursor (Polymorphic membrane
DE protein G).
GN PMPG OR C7871.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
RX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kalmán S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -|- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; AB001360; AAC68469.1; -
 DR PIR; G71460; G71460;
 DR PHCI-2DPAGE; O84879; -
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; DUPL45; 1.
 DR TIGRfams; TIGR01414; autotrans_bar1; 1.
 DR TIGRfams; TIGR01376; POMP_repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 1013 PROBABLE OUTER MEMBRANE PROTEIN PMPG.
 SQ SEQUENCE 1013 AA; 107366 MW; F0927743C0A651DD CRC64;

Alignment Scores:

Pred. No.: 4,77e-60 Length: 1013
 Score: 1120.50 Matches: 313
 Percent Similarity: 44.66% Conservative: 160
 Best Local Similarity: 29.56% Mismatches: 409
 Query Match: 20.72% Indels: 177
 DB: 1 Gaps: 33

US-09-428-122-1 (1-3000) x PMPG_CHLTR (1-1013)

QY 101 ATGAAGTCTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTCCCTTTGTTCTATG 160
 DB 1 MetGlnThrSerPheHisLysPheLeuSerMetIleLeuAlaTyrSerCysSer 20
 QY 161 ATTGCT-----ACCGACAGTGTTCGATTCAGTTCGAGTTTCGATGGAAT 208
 DB 21 LeuSerGlyGlyTyrAlaAlaGluIleMetIleProGlnGlyIleTyrAspGlyGlu 40
 QY 209 AAA---AATGGTAATTTTTCAGTTCGTGAGTCAGTCAGGAAGATCGTGAATCTACCTA 255
 DB 41 ThrLeuThrValSerPheProTyrThrValIleGlyAspProSerGlyThrThrValPhe 60
 QY 266 TTTAAGGGAATGTCACCTAGAAATATTCCTGGAACAGCAGCAGCAATCACAAAAGC 325
 DB 61 SerAlaGlyGluLeuThrLeuLysAsnLeuAspAsnSerIleAlaAlaLeuProLeuSer 80
 QY 326 TGTTTTAACAACTAAGGCGATTGACTTTACAGTAACGGAATCTCTATTGTTTC 385
 DB 81 CysPheGlyAsnLeuLeuGlySerPheThrValLeuGlyArgGlyHisSerLeuThrPhe 100
 QY 386 CAAACGCTGATCAGGAGCTGTAGCAGGGCTGCTGTTAACAGCAGCGGTGTAGATAAA 445
 DB 101 GluAsnIleArgThrSerThr---AsnGlyAlaAlaLeuSerAspSerAlaAsnSerGly 119
 QY 446 TCTACCACTGTTATAGGGTTTCTTCGCTATCTTTT----- 481
 DB 120 LeuPheThrIleGluGlyPheLysGluLeuSerPheSerAsnCysAsnSerLeuLeuAla 139
 QY 482 -----ATTCCGCTCTCTGGAAGTTTCGATAACTACC 511
 DB 140 ValLeuProAlaAlaThrThrAsnAsnGlySerGlnThrProThrThrSerThrPro 159
 QY 512 GGCAAGGCGGTAGTCTCTACGGTAGCTTGTAGTTGACAAAATGTCAGTTG 571
 DB 160 SerAsnGlyThrIleTyrSerLysThr---AspLeuLeuLeuLeuAsnAsnGluLysPhe 178
 QY 572 CTCCTTCAGCAAAACTTTTCAACCGATAATGGCGGTCTATCACCGCAAAACTCTTTCA 631
 DB 179 SerPheTyrSerAsnLeuValSerGlyAspGlyAlaIleAspAlaLysSerLeuThr 198
 QY 632 TTAACAGGACTACAATGTACGCTCTGTTTCTGAAATACCTCTCAAGAAAGGCGGA 691
 DB 199 ValGlnGlyIleSerLysLysCysValPheGlnGluAsnThrAlaGlnAlaAspGlyGly 218

QY 692 GCCATTCCAGACTTCGATCCGCTTACCATTACTGGAACCAAGGGAAGTCTCTTT--- 748
 DB 219 AlaCysGlnValValThrSerPheSerAlaMetAlaAsnGluAlaProIleAlaPheIle 238
 QY 748 ----- 748
 DB 239 AlaAsnValAlaGlyValArgGlyGlyIleAlaAlaValGlnAspGlyGlnGlnGly 258
 QY 749 -----TCTGCAATCTCTTCGATTCT----- 772
 DB 259 ValSerSerSerThrThrGluAspProValValSerPheSerArgAsnThrAlaVal 278
 QY 773 -----GGAGCTGCAATTTTACAGAGCCTCGGTGACT 805
 DB 279 GluPheAspGlyAsnValAlaArgValGlyGlyIleTyrSerTyrGlyAsnValAla 298
 QY 806 ATTTCTTAATAGTCTAAAGTTTCCTTTATGTACAAT----- 841
 DB 299 PheLeuAsnAsnGlyLysThrLeuPheLeuAsnValAlaSerProValTyrIleAla 318
 QY 842 -----AGGTCACAGGAGCGAGCTCTCAACACAGGGGGATAG-----TCAGAGGT 889
 DB 319 AlaGluGlnProThrAsnGlyGlnAlaSerAsnThrSerAspAsnTyrGlyAspGlyGly 338
 QY 890 GCTATC---TGT-----GCTTATAAACTAGTACAGATTAAGGTCAAC 931
 DB 339 AlaIlePheCysLysAsnGlyAlaGlnAlaAlaGlySerAsnAsnSerGlySerValSer 358
 QY 932 CTCACCTGGAATCAGATGTTCTCTCAACAATATACATCAACACAGCGGAGAGT 991
 DB 359 PheAspGlyGluGlyValValPhePheSerSerAsnValAlaAlaGlyLysGlyAla 378
 QY 992 ATCTATGTAAAAGCTCGAAGTCTCCGAGGACTTACCTATTCTAGTAAATAGT 1051
 DB 379 IleTyrAlaLysLysLeuSerValAlaAsnCysGlyProValGlnPheLeuGlyAsnIle 398
 QY 1052 GTCAATGGAGGTACAGCTCTCTAAAGTGGAGCATAGTATCGAAGATGCGGGAATG 1111
 DB 399 AlaAsn-----AspGlyGlyAlaIleTyrLeuGlyGluSerGlyGluLeu 413
 QY 1112 AGTTTATCCCGCATAGTGTGACATTTCTTTTAGGGAAT-----ACAGTCACT 1162
 DB 414 SerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsnLeuLysArgThrAlaLys 433
 QY 1163 TCTACTACTCTCTGGGAGAAAT-----AGAAGTAGTATCGACTTAGAACG 1207
 DB 434 GluAsnAlaAlaAspValAsnGlyValThrValSerSerGlnAlaIleSerMetGlySer 453
 QY 1208 AGTGCAAGATGACAGCTTTGCGTCTGCTGTGTGTAGAGCCATCTCTTATGATCC 1267
 DB 454 GlyGlyIleIleThrThrLeuArgAlaLysAlaGlyHisGlnIleLeuPheAsnAspPro 473
 QY 1268 ATAACCTACAGGATTCATCCCAACA-----GTTACAGATGCTTTAAAGTTAAT 1315
 DB 474 IleGluMetAlaAsnGlyAsnAsnGlnProAlaGlnSerSerGluProLeuLysIleAsn 493
 QY 1316 GAGACTCCGCGAGATCTGCCTACATATACAGGAAACATCATCTCTCAGAGAAAAG 1375
 DB 494 AspGlyGluGly-----TyrThrGlyAspIleValPheAla----- 505
 QY 1376 TTATCAGACAGACAGCGCGAGATTCATAAAATCTTACTTCGAAGCTACTACAGCCTGTA 1435
 DB 506 -----AsnGlyAsnSerThrLeuTyrGlnAsnVal 515
 QY 1436 ACTCTTTTCAGGAGTACTCTATCTTTTAAACATGGAGTACTCTCTCAGACTCAGGATTC 1495
 DB 516 ThrIleGluGlnGlyArgIleValLeuArgGluLysAlaLysLeuSerValAsnSerLeu 535
 QY 1496 ACTCAACAGCAGCAATCTCGTCTCGAAATAGGAGCTAGGAACTACTCTAGAA----- 1546
 DB 536 SerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySerThrLeuAspPheValThr 554
 QY 1547 -----CCTGCTGATACTAGC-----ACCATAAACAATTTGGTC 1579

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Db      555 ProGlnProProGlnGlnProProAlaAlaAsnGlnLeuLeuThrLeuSerAsnLeuHis 574
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1580 ATTAACATCAGTCTCTATA-----GACGGTGCA-----1606
Db      575 LeuSerLeuSerLeuLeuAlaAsnAsnAlaValThrAsnProProThrAsnProPro 594
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1607 -----AAGAGCGAAAAATAGAACCAAGCTACGTCAAAAATCTGACTTTATCT 1657
Db      595 AlaGlnAspSerHisProAlaIleIleGlySerThrThrAlaGlySerValThrIleSer 614
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1658 GGAACCATCAGTCTTTATGACCGGACGGGACGGTCTTATGAAAATCATAGT---TTAAGA 1714
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QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1715 AATCTCTCAGTCTACACATCTTAGAGCTCAAGCTCTCGAAAGCTCTGAACTGTAACAGCACCGCA 1774
Db      635 SerAsnGlnLysIleAspValLeuLysLeuGlnLeu---GlyThrGlnProSerAlaAsn 653
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1775 GTGACTCCAGATCCCTATAATAGGGTGAGAAATTC---CATTACGGCTATCAGGGAATCTGG 1831
Db      654 AlaProSerAspLeuThrLeuGlyAsnGluMetProLysThrGlyTyrglnGlySerTrp 673
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1832 GCCCAATGTTGGGGACAGGGGCTCTACAGCTGCAACCTC-----AAC 1879
Db      674 ---LysLeuAlaIleAspProAsnThrAlaAsnAsnGlyProIleThrLeuLysAlaThr 692
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1880 TGGACTAAACAGTGGTATATCTCTATCCGAGCGGTATCGGCTCTTTAGTCCCTAATAGC 1939
Db      693 TrpThrLysThrGlyTyrglnGlyProGluArgValAlaSerLeuValProAsnSer 712
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1940 TTATGAATGCAATTAAGATATAGTCTCTCTCCATTATCTTATGGAGACTGCAACGAA 1999
Db      713 LeuTrpGlySerIleLeuAspIleArgSerAlaHisSerAlaIleGlnAlaSerValAsp 732
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2000 GGGTTCAGGGAGACGGTCTTTGGTGTGCTGATTAATCTTAACTCTTCCATAAGAT 2059
Db      733 GlyArgSerTyrcysargglyLeuIleIleIleIleIleIleIleIleIleIleIleIle 752
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2060 AGTCAAAAACACGACGGGTTTCGCCATTTGAGTGGCGGTATGCTCATAGAGAGAAC 2119
Db      753 ArgAspAlaLeuGlyGlnGlyTyrglyTyrglyTyrglyTyrglyTyrglyTyrglyTyrgly 772
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2120 CTACATCTGTTTCAGATTAAGATCTTAGTGTGCTGATTTGTCAGCTCTTTGAGAGAT 2179
Db      773 SerTyrglySer---SerMetPheGlyLeuAlaPheThrGluValPheGlyArgSer 791
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2180 AGAGACTCTTTGAGTAAAGATCAAGGTACAGTCTACGGAGGAAGTCTCTATTACCAG 2239
Db      792 LysAspTyrglyValValCysArgSerAsnHisAlaCysIleGlySerValTyrgly 809
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2240 CACAAGAAACCTATATCTCTCTCTGCAAACTACGGCTTGTGTGTTGTTATGTT 2299
Db      810 -----LeuSerThrLysGlnAlaLeuLysCysgly---SerTyrgly--- 820
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2300 CCTACAGAGATTCCTGTTCTCTCTTTTCAGGA-----AAGTCTAGCTACCCCATAGC 2350
Db      821 -----LeuPheGlyAspAlaPheIleArgAlaSerTyrglyPheGly 834
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2351 GATAACGATCTGAAAACCAAGATATACACATATCTCTGTTAAAGGAAGCTGGGGGAAT 2410
Db      835 AsnGlnHisMetLysThrSerTyrglyThrPheAlaGluSerAspValArgTrpAspAsn 854
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2411 GATAGTTTCGCTTTAGAAATTCGGTGGAGAGCTCCGATTGCTTAGATGAAGTGTCTTA 2470
Db      855 AsnCysLeuValGlyGluIleGlyValGlyLeuProIleValIleThrProSerLysLeu 874
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2471 TTT---GAGCAGTACATGCGCTTCATGAAATTCAGTTGCTCTATGCATCATCAGGAGGT 2527
Db      875 TyrLeuAsnGluLeuArgProPheValGlnAlaGluPheSerTyrglyAlaAspHisGluSer 894
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2528 TTTAAGACACAGGACAGAGCTGCTGATTTGGAGTAGCGCTTGTGATCTTGGC 2587

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Db      895 PheThrGluGluGlyAspGlnAlaArgAlaPheArgSerGlyHisLeuMetAsnLeuSer 914
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2588 TTACTATCGGATCCGATTTGATAAGGAATCAAGACTCCCAAGATGCAACGTACAATCTA 2647
Db      915 ValProValGlyValLysPheAspArgCysSerThrHisProAsnLysTyrglySerPhe 934
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2648 ACTCTGTTGTTACTGTGGATCTTGTTCGTAGTAACCCGACTGTACGACACACTGCGA 2707
Db      935 MetGlyAlaTyrlleCysAspAlaTyrglyThrIleSerGlyThrGlnThrThrLeuLeu 954
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2708 ATTACGGGTGATTTGGAACACCTTCGTTACGATTTGGCAAGTTCAGTTCCTT 2767
Db      955 SerHisGlnGluThrTrpThrThrAspAlaPheHisLeuAlaArgHisGlyValIleVal 974
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2768 CGTCAGGGAACCACTTTTGTCTTTAACTCAAAATTTTGAAGCTTTAGCAATTTCTTT 2827
Db      975 ArgGlySerMetTyrglyAlaSerLeuThrSerAsnIleGluValTyrglyHisGlyArgTyrgly 994
QY      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2828 GAATTCGCTGGTCTATCTCGCAATTAACAATGAGTCTAGACTTAGGAGCAAAATACCAATTC 2884
Db      995 GluTyrglyAspThrSerArgGlyTyrglyLeuSerAlaGlySerLysValArgPhe 1013

RESULT 11
PMFG CHLMU
ID PMFG CHLMU STANDARD; PRT; 987 AA.
AC Q9PU45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmgG precursor (Polymorphic membrane
DE protein G).
GN PMG OR TC0263.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC
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CC
CC EMBL; AE002293; AAF39132.1; -.
CC PIR; H81722; H81722.
CC TIGR; TC0263;
CC InterPro; IPR006315; Autotransport.
CC InterPro; IPR005546; Autotransporter.
CC InterPro; IPR003368; Chlamydia PM.
CC Pfam; PF03797; Autotransporter; 1.
CC Pfam; PF02415; DUF145; 1.
CC TIGRFAMs; TIGR01414; autotrans_bar1; 1.
CC TIGRFAMs; TIGR01376; POMP_repeat; 6.
CC Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 987 PROBABLE OUTER MEMBRANE PROTEIN PMPG.
FT SEQUENCE 987 AA; 104867 MW; 32079BD6BEB2DA42 CRC64;
SQ

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Alignment Scores:

Pred. No.: 7,11e-56 Length: 987
 Score: 1051.00 Matches: 294
 Percent Similarity: 43.20% Conservative: 154
 Best Local Similarity: 28.35% Mismatches: 429
 Query Match: 19.43% Indels: 160
 DB: 1 Gaps: 26

US-09-428-122-1 (1-3000) x PMPG_CHLMU (1-987)

QY 101 ATGAAGTCTCTTCTCCCAAGTTGTATTTCTACATTTGCTATTATTTCCCTTTGCTATG 160
 DB 2 MetGlnThrProPheHisLysPhe-----PheLeuLeuAlaMet 14
 QY 161 ATTGCTACCGAGACAGTTTGGATTCAAGTGCAGT----- 196
 DB 15 LeuSerTyrSerLeuLeuGlnGlyHisAlaAlaAspIleSerMetProGlyIle 34
 QY 197 TTCGATGGGAATAAA---AATGGTAATTTTTCAGTTTCGTGAGAGTCAGGAAGATGCTGA 253
 DB 35 TyrAspGlyThrThrLeuThrAlaProPheProTyrThrValIleGlyAspProArgGly 54
 QY 254 ACTACCTACCTATTAAAGGAATATGCTCTAGAAAATATTCCTGGAACAGCCAGCA 313
 DB 55 ThrLysValThrSerSerGlySerLeuLeuLeuLysAsnLeuAspAsnSerIleAlaThr 74
 QY 314 ATCACAAAAAGCTGTTTAAACACTAAGCGCGATTTCAGTTTTCAGGTAACGGGAAC 373
 DB 75 LeuProLeuSerCysPheGlyAsnLeuLeuGlyAsnPheThrIleAlaGlyArgGlyHis 94
 QY 374 TCTCTATTGTTCCAAACGGTGATGCGAGGAGTGTAGCAGGGCTGCTGTTAAACAGCAGC 433
 DB 95 SerLeuValPheGluAsnIleArgThrSerThr---AsnGlyAlaAlaLeuSerAsnHis 113
 QY 434 GTGGTAGATAAACTACCAGCTTTATAGGTTTCTTCGTATCTTTATT----- 484
 DB 114 AlaProSerGlyLeuPheValIleGluAlaPheAspGluLeuSerLeuLeuAsnCysAsn 133
 QY 485 -----GCGTCTCTGGAAGTTTCGATACTACCGCAAAAGGAGCC 523
 DB 134 SerLeuValSerValValProGlnThrGlyGlyThrThrThrSerValProSerAsnGly 153
 QY 524 GTTAGCTGCTCTACGGGTAGCTTGTGACAAAAAATGCTATGCTTCTTCAGCAAA 583
 DB 154 ThrIleTyrSerArgThrAspLeuValLeuArgAspIleLysLysValSerPheTyrSer 173
 QY 584 AACTTTTCAACGGATAATGGGGTGTCTATCACCGCAAAACTCTTTTCATTAAACAGGACT 643
 DB 174 AsnLeuValSerGlyAspGlyGlyAlaIleAspAlaGlnSerLeuMetValAsnGlyIle 193
 QY 644 ACAATGTCAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTTCAGACT 703
 DB 194 GluLysLeuCysThrPheGlnGluAsnValAlaGlnSerAspGlyGlyAlaCysGlnVal 213
 QY 704 TCCGATGCCCTTACCATCTACTGGAACCAAGGGAGTCTCTTTTCTGACATCTTCT 763
 DB 214 ThrLysThrPheSerAlaValAlaGlyAsnLysValProLeuSerPheLeuGlyAsnValAla 233
 QY 764 TCGGATCTCGAGCTGCNAAT-----TTTACA 790
 DB 234 GlyAsnLysGlyGlyGlyValAlaAlaValLysAspGlyGlnGlyAlaGlyGlyAlaThr 253
 QY 791 GAAGCTCGGGTACTATTCTTAATAATGCTAAAGTTTCTTTTATGCAATTAAGTCT--- 847
 DB 254 AspLeuSerValAsnPheAlaAsnAsnThrAlaValGluPheGluGlyAsnSerAlaArg 273
 QY 848 ACAGGAGCGAGCTCTCTCAACACCGGGGATATGTCA----- 883
 DB 274 IleGlyGlyGlyIleTyrSerAspGlyAsnIleSerPheLeuGlyAsnAlaLysThrVal 293
 QY 883 ----- 883

DB 294 PheLeuSerAsnValAlaSerProIleTyrValAspProAlaAlaAlaGlyGlyGlnPro 313
 QY 884 -----GGAGTGTCTATCTGTGCTTTATAAACAATAGTACA 916
 DB 314 ProAlaAspLysAspAsnTyrGlyAspGlyGlyAlaIlePheCysLysAsnAspThrAsn 333
 QY 917 GATACTAAGTTCACCTCAGTGAATCAGATGTTACTTCTCAGCAACAATACATCGACA 976
 DB 334 IleGlyGluValSerPheLysAspGluGlyValValPhePheSerIleAsnIleAlaAla 353
 QY 977 ACACGGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTTCGAGGAGCTTACCCCTA 1036
 DB 354 GlyLysGlyGlyAlaIleTyrAlaLysLysLeuThrIleSerAspCysGlyProValGln 373
 QY 1037 TTCAGTAGAATAGTGTCAATCGAGGTACAGTCCCTAAAGGTGGAGCCATAGCTATCGAA 1096
 DB 374 PheLeu-----GlyAsnValAlaAsnAspGlyGlyAlaIleTyrLeuVal 388
 QY 1097 GATAGTGGGAATTCAGTTTATCCGCCGATAGTGTGATGTCATTGCTTTTAGGATACA 1156
 DB 389 AspGlnGlyGluLeuSerLeuSerAlaAspArgGlyAspIleIlePheAspGlyAsnLeu 408
 QY 1157 GTCACCTTCTACTACTCTCTGG-----ACGAATAGAACTAGT 1192
 DB 409 LysArgMetAlaThrGlnGlyAlaAlaThrValHisAspValMetValAlaSerAsnAla 428
 QY 1193 ATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCTGCTGCTGCTGCTGAGCCATC 1252
 DB 429 IleSerMetAlaThrGlyGlyGlnIleThrThrLeuArgAlaLysGluGlyArgArgIle 448
 QY 1253 TACTCTATGATGCCATACTACAGATCATCCACAACAGTTACAGATGCTCTTAAAGTT 1312
 DB 449 LeuPheAsnAspProIleGluMetAlaAsnGlyGlnProValIleGlnThrLeuThrVal 468
 QY 1313 AATGAGACTCCGCGAGATTCTGCACTACAAATATACAGGGAACATCATCTTTCAGAGAA 1372
 DB 469 AsnGluGlyGluGly-----TyrThrGlyAspIleValPhe----- 480
 QY 1373 AAGTTATCAGACAGAGCGCCGAGATCTCTAAATCTTACTTCTGAAAGCTACTACAGCT 1432
 DB 481 -----AlaLysGlyAspAsnVal-----LeuTyrSerSer 490
 QY 1433 GTAACCTTTTCAGGAGTACTCTATCTTTAAACATGGAGTGACTCTCGCAGACTCAGGCA 1492
 DB 491 IleGluLeuSerGlnGlyArgIleIleLeuArgGluGlnThrLysLeuLeuValAsnSer 510
 QY 1493 TTCACCTCAACAGCAGCATCTCTGCTCGAAATGGACGTAGGAACTACTCTAGAA----- 1546
 DB 511 LeuThrGlnThrGlyGlySer---ValHisMetGluGlyGlySerThrLeuAspPheAla 529
 QY 1547 -----CCTGCTGATCTAGCACCATTAACAAATTTGTCATTAACATCAGT 1591
 DB 530 ValThrThrProProAlaAlaAsnSerMetAlaLeuThrAsnValHisPheSerLeuAla 549
 QY 1592 TCTATA-----GACGTCGCAAAAG-----GCAAAATAGAA 1624
 DB 550 SerLeuLeuLysAsnAsnGlyValThrAsnProProThrAsnProProValGlnValSer 569
 QY 1625 ACCAAAGCTACGTCAAAAAAT-----CTGACTTTTCTGGAACCATCAGT 1669
 DB 570 SerProAlaValIleGlyAsnThrAlaAlaGlyThrValThrIleSerGlyProIlePhe 589
 QY 1670 TTATGGACCCGACGGCGACGTTTATGAAATCATAGT---TTAGAATCTCTAGTCC 1726
 DB 590 PheGluAspLeuAspGluThrAlaTyrAspAsnAsnGlnIlePheGlyAlaAspGlnThr 609
 QY 1727 TAGCATCTTAGAGCTCAAGCTTCTGGAACTGTAAACAGCACCCAGTGCATCCAGAT 1786
 DB 610 IleAspValLeuGlnLeuHisLeuGlyAlaAsnProProAlaAsnAlaProThrAspLeu 629
 QY 1787 CCTATATGGGTGAGAAATTCATATACGGCTATCAGGAACTTGGGCGCCCAATTTGTTGG 1846
 DB 630 ThrLeuGlyAsnGluSerSerLysTyrGlyGlnGlySerTrp---ThrLeuGlnTrp 648

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RESULT 12
PMPI_CHLMU
ID PMPI_CHLMU STANDARD; PRT; 867 AA.
AC Q9PLA1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmpl precursor (Polymorphic membrane
protein 1).
GN PMPI OR TC0267.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Ni99;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39."
RT Nucleic Acids Res. 28:1397-1406(2000).
RL Nucleic Acid Res. 28:1397-1406(2000).
CC -|- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC -|- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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or send an email to license@isb-sib.ch).
DR EMBL; AE002294; AAF39136.1; -.
DR F81721; F81721.
DR TIGR; TC0267; -.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 29
FT CHAIN 30 867
FT SEQUENCE 867 AA; 95017 MW; 557994185A9B5652 CRC64;
SQ SEQUENCE 867 AA; 95017 MW; 557994185A9B5652 CRC64;
Alignment Scores:
Pred. No.: 1.79e-47 Length: 867
Score: 911.00 Matches: 281
Percent Similarity: 44.60% Conservative: 144
Best Local Similarity: 29.49% Mismatches: 384
Query Match: 16.84% Indels: 144
Gaps: 30
US-09-428-122-1 (1-3000) x PMPI_CHLMU (1-867)
QY 149 CTTTGTCTATGATTCACGAGACAGTTCGATTCAGTCGAGTTTCGATGGGAA 208
Db 18 ProThrAlaIleuPheGlyGlnAspAlaLeuAspLysSerAlaLeuIleThrLysAsn 37
QY 209 AAAATGGT-----AATTTTCA----- 226
Db 38 ProAsnSerIleValCysThrPheLeuGluAspCysThrMetGluAsnPheSerProAla 57
QY 227 ---GTTCTGTGAGCTCAGGAGAT-----GCTGGACTACCTACTATT 268
Db 58 LeuLeuSerHisAlaArgGlnAspProLeuTyrllelleGlyAsnThrHis----- 75
QY 269 AAGGAAATGTCACTCTAGAAAATATT---CCTGGAACAGGCACAGCAATCACAAGAGC 325
Db 76 -----AsnTrpPheValSerAsnLeuHisProSerThr-----AsnGluGlu 89
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Db	716	GlulIcGlyAlaSerIleProIleValSerAsnGlySerGlyLeuPheSerPheSer	735
QY	2486	CCCTTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACA	2545
Db	736	IlePheSerLysLeuGlnGlyPheSerGlyLysGlnAspGlyPheGlnGluSerArgGly	755
QY	2546	GAAGCTCGTGAATTTGGAAGTAGCCGCTCTTGTGAATCTTCCTTACCTACGCGGATCCGA	2605
Db	756	GluAlaArgAlaPheAlaAspSerSerPheThrAsnIleSerLeuProValGlyIleAla	775
QY	2606	TTTGATTAAGAAATCAGACTGCCAGATGCACATCACTTAACCTCTGCTTATCTGTG	2665
Db	776	PheGluLysLysSerGlnLysThrArgAsnTyrTyrHisPheLeuGlyAlaTyrIleGln	795
QY	2666	GATCTTCTTCGTAGTAACCCCGACTGTGACAGCAACACTGCGAATTACGCGTGATTCCTGG	2725
Db	796	AspLeuLysArgCysValGluSerGlyProValThrLeuLeuLysAsnSerValThrTrp	815
QY	2726	AAAACCTTCGCTACGAAATTTGGCAAGACAAGCTTTAGTCCTCTCGTCAGGAACCAATTTT	2785
Db	816	AspAlaProMetAlaAsnLeuLeuAspSerArgAlaTrpMetPheArgLeuThrAsnGlnArg	835
QY	2786	TGCTTTAACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTCACT	2845
Db	836	AlaLeuHis---ArgPheGlnThrLeuValAsnMetSerTyrMetLeuArgGlyGlnSer	854
QY	2846	CGCAATTTACAATGTAGACTTAGGAGCAAAATACCAATTC	2884
Db	855	TyrSerTyrSerLeuAspLeuGlyThrThrTyrArgPhe	867
RESULT 13			
PMPI	CHLTR		
ID	PMPI	CHLTR	STANDARD; PRT; 878 AA.
AC	O84882;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, last sequence update)	
DT	16-OCT-2001	(Rel. 40, last annotation update)	
DE	Probable outer membrane protein pmpl precursor (Polymorphic membrane protein 1).		
DE	PMPI OR CT874.		
OS	Chlamydia trachomatis.		
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.		
CC	NCBI	TaxID=813;	
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=D/UK-3/Cx;		
RX	MEDLINE=9900809;	PubMed=9784136;	
RA	Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,		
RA	Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,		
RA	Davis R.W.;		
RT	"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis".		
RL	Science	282;754-759(1998).	
CC	-1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).		
CC	-1- SIMILARITY: BELONGS TO THE PMW OUTER MEMBRANE PROTEIN FAMILY.		
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DR	EMBL;	AE001361; AAC68472.1; -.	
DR	PIR;	B71460; B71460.	
DR	InterPro;	IPR003368; Chlamydia_PMP.	
DR	Pfam;	PF02415; DUF145; 1	
DR	TIGRFAMs;	TIGR01376; POMP repeat; 6.	
KW	Outer membrane; Signal; Multigene family; Complete proteome. FT SIGNAL 1 24 POTENTIAL.		

1274	QY	ACAGGATCATCCACAA	CAGTTACAGATGCTTTAAAGTGTAAATGAGACTCGGCAGATTCT	1333
357	Db	GlnGluSerSer	-----LysGluSerProLeuProSer	368
1334	QY	GCACCTACATATACA	-----	1348
369	Db	SerLeuGlnAlaSerVal	ThrSerProThrProAlaThrAlaSerProLeuValIleGln	388
1349	QY	-----GGAAACATCATCTT	CCACGAGAGAAAGTTATCCAGAGACAGAGCCGCA	1396
389	Db	ThrSerAlaAsnArgSerVal	IlePheSerSerGluArgLeuSerGluGluGluTysThr	408
1397	QY	GATTCTAAAATCTTACTT	CGAAGCTACTACAGCTCTAACTCTTTCAGGAGTACTCTTA	1456
409	Db	ProAsp	---AsnLeuThrSerGlnLeuGlnProIleGluLeuLysSerGlyArgLeu	427
1457	QY	TCTTTAAACATGGAGTGACTCT	CGACACTCAGGCATTCACCAACAGGCAGATTCTCGT	1516
428	Db	ValLeuLysAspArgAla	ValLeuSerAlaProSerLeuSerGlnAspProGlnAlaLeu	447
1517	QY	CTCGAAATGGACGTAGGAAC	TACTCTAGAACCTGCTGATACTACTACACCAATAAATTTG	1576
448	Db	LeuIleMetGluAlaGly	ThrSerLeuLysThrSerSerAspLeuLysLeuAlaThrLeu	467
1577	QY	GTCATTAAATCATGTTCT	TATAGACGGTGCAAGAGCCAAATAGAACCAAGCTACG	1636
468	Db	SerIleProLeuHisSerLeu	AspThrGluLysSerValThrIleHis	483
1637	QY	TCMAAAATCTGACTTTATCT	TGGAACCATCACTTTATTGGACCCGACGGCACTTTTAT	1696
484	Db	AlaProAsnLeuSerIle	GlnLysIlePheLeuSerAsnSerGlyAspGluAsnPheTyr	503
1697	QY	GAAATCATAGTTTAAAGAAAT	CCCTCAGCTCTACACATCTTAGAGCTCAAGCTCTCGGA	1756
504	Db	GluAsnValGluLeuLeu	SerLysGluGlnAsnIleProLeuLeuThrLeuSer	522
1757	QY	ACTGTAAACAGCACCGCAG	TCCAGATCCTTAATATGGTGAGAATTCCTATTACGC	1816
523	Db	LysGluGlnSerHisLeu	HisLeuProAspGlyAsnLeuSerSer	540
1817	QY	TATCAGGNACTTGGGGCCCA	ATTGTTGG-----GGGACAGGGCTCTACGACT	1867
541	Db	TyrGlnGlyAspTyr	---ThrPheSerTyrLysAspSerAspGluGlyHisSerLeuIle	559
1868	QY	GCAACCTTCAACTGGACT	TAATAACTTCTAATCCGACGCTATCGGCTCTTTA	1927
560	Db	Ala	-----AsnTyrThrProLysAsnTyrValProHisProGluArgGlnSerThrLeu	577
1928	QY	GTCCCTAATAGCTTATGA	ATGCAATTTAGATATTAGCTCTCTCCATATCTTATATGGAG	1987
578	Db	ValAlaAsnThrLeuTyr	AsnThrTyrSerAspMetGlnAlaValGlnSerMetIleAsn	597
1988	QY	ACTGCAACAGGAGGCTT	CGAGGACCGTCTTT-----TGCTGTGGATTATCT	2041
598	Db	ThrIleAlaHisGly	-----GlyAlaTyrLeuPheGlyThrTyrGlySerAlaValSer	615
2042	QY	AACTTCTTC-----CATA	AGGATAGTACAAAACACACGCGGGTCTTCGCAATTCAGT	2095
616	Db	AsnLeuPheTyrAlaHis	AspSerSerGlyLysProIleAspAsnTyrHisHisArgSer	635
2096	QY	GGCGTTATGTCAATAGG	AGAAACCTCACTACTGTTCCAGATATAGATTCCTAGTGCTGCA	2155
636	Db	LeuGlyTyrLeuPheGly	IleSerThrHisSerLeuAspAspHisSerPheCysLeuAla	655
2156	QY	TTTTGTCACTCTTTGGA	AGATAGACACTTGTGTAGTCTAGAAATCAAGGTACAGTC	2215
656	Db	AlaGlyGlnLeuLeuGly	LysSerSerPheIleThrSerThrGluThrThrSer	675
2216	QY	TACGGAGGAACCTCTCT	TATTACCAGCACACAAACCTATATCTCTCTCTTCTGCAACTA	2275
676	Db	TyrIleAlaThrValGln	AlaGln-----LeuAlaThrProLeu	688
2276	QY	CGSCCTTGTTCGTGTCT	TATGTTCTCTACAGAGATTCCTGTCTCTTTTCAGGAAACCTT	2335

D	b	689	- - - - -MetLysIleSerAlaGlnAla	695
Q	y	2336	AGCTACACCATACGGATAACGCATCGATTGAACAACCAAGTATACACATCTACTGTGTTAA	2395
D	b	696	CysTy rAsnGluSerIleHisGluLeuLysThrLysTy rArgSerPheSerLysGluGly	715
Q	y	2396	-- --GGAAGCTGGGGAGATAGTAGTTTCGCTTTAGAATTCGGTGGAGAGAGCTCCGATTGCG	2452
D	b	716	PheGlySerTrpHisSerValAlaValSerGlyGluValCysAlaSerIleProIleVal	735
Q	y	2453	TTCATGAAAGTGCTCTATTGTGAGCAGTACATGCCCTTCATGAAATTCAGATTGCTCTAT	2512
D	b	736	SerAsnGlySerGlyLeuPheSerSerPheSerIlePheSerLysLeuGlnGlyPheSer	755
Q	y	2513	GCACATCAGGAAGGTTTTTAAGAACACAGGACACAGAGCTCGTGAATTTGGAAAGTAGCCGT	2572
D	b	756	GlyThrGlnAspGlyPheGluGluSerSerGlyGluIleArgSerPheSerAlaSerSer	775
Q	y	2573	CTTGTGAATCTTGCTTACCTATCGGATCCGATTTCGATTGATAGGAATCAGACTGCCAGAT	2632
D	b	776	PheArgAsnIleSerLeuProMetGlyIleThrPheGlnLysSerGlnLysThrArg	795
Q	y	2633	GCAACGTACATCTAATCTCTTGTTTACTGTGTGATCTTGTTCTAGTAAACCCGACTGT	2692
D	b	796	AsnTy rTy rTy rPheLeuGlyAlaTy rIleGlnAspLeuLysAlaGspValGluSerGly	815
Q	y	2693	ACGACAACACTCGCAATTAGCGGTGATCTTGGAAAACTTCGTACGAATTTGGCAAGA	2752
D	b	816	ProValValLeuLeuLysAsnAlaValSerTrpAspAlaProMetaLaAsnLeuAspSer	835
Q	y	2753	CAAGCTTTAGTCCTTCGTGFCAGGGAACCATTTTTCCTTAACCTCAAATTTTGAAGCCTT	2812
D	b	836	ArgAlaTy rMcPheArgLeuThrAsnGlnArgAlaLeuHis-- --ArgLeuGlnThrLeu	854
Q	y	2813	AGCCAATTTCTTTTGAATTCGCTGGGTGTCATTCGCAATTACAATTAGACTTTAGGACGA	2872
D	b	855	LeuaenValSerTy rValLeuArgGlyGlnSerHisSerTy rSerLeuAspLeuGlyThr	874
Q	y	2873	AAATACCAATTC	2884
D	b	875	ThrTy rArgPhe	878
 RESULT 14 PM21 CHLPN STANDARD; PRT; 1609 AA. AC Q9Z6U5; Q9RB58; DT 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Probable outer membrane protein pmp21 precursor (Polymorphic membrane protein 21). DE FMP21 OR CPN0963 OR CP0897. GN Chlamydia pneumoniae (Chlamydophila pneumoniae). OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila. OX NCBI_TaxID=83558; RN [1]_TaxID=83558; RP SEQUENCE FROM N.A. RC STRAIN=CWL029; RX MEDLINE=E9920606; PubMed=10192388; RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger K., Grimwood J., Davis R.W., Stephens R.S.; RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999). RL [2] RN SEQUENCE FROM N.A. RP STRAIN=AR39; RC MEDLINE=20150255; PubMed=10684935; RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman K., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Bisen J., Fraser C.M.;				

RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138.
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC
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 CC
 DR EMBL; AE001676; AAD19099.1; -;
 DR EMBL; AE002248; AAF38684.1; -;
 DR EMBL; AP002548; BAA99171.1; -;
 DR PIR; A86611; A86611.
 DR PIR; H72013; H72013.
 DR PHCI-2DPAGE; Q9RB58; -;
 DR TIGR; CP0897; -;
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF01797; Autotransporter; 1.
 DR Pfam; PF02415; DUF145; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 13.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 30
 FT CHAIN 31 1609 PROBABLE OUTER MEMBRANE PROTEIN PMP21.
 FT CONFLICT 420 420 I -> M (IN REF. 3).
 SQ SEQUENCE 1609 AA; 170865 MW; 2604C3E9FC4024CB CRC64;
 Alignment Scores:
 Pred. No.: 7,05e-34 Length: 1609
 Score: 685.50 Matches: 254
 Percent Similarity: 38.91% Conservative: 144
 Best Local Similarity: 24.81% Mismatches: 372
 Query Match: 12.67% Indels: 253
 DB: 1 Gaps: 36
 US-09-428-122-1 (1-3000) x PM21_CHLPN (1-1609)
 QY 278 GTCACCTAGAAAATATTCCTGGACAGGACGACGCAATCACAAAAGCTGTTT----- 331
 DB ValSerSerThrAspIleArgGlyGlyAlaIleLeuAlaGlnHisIlePheThr 705
 QY 332 AACACACTAAGGCGATTGACTTTCACAGGTACGGGAACCTCTCTATTGTTCCAAACG 391
 DB AspAsnThr---GlyAsnLeuArgPheSerGlyAsn----- 716
 QY 392 GTGGATGACGGAGCTGTAGCGGGCTGCTGTAAACAGACAGCGTGGTGTAGATAAATCTACC 451
 DB -----LeuGlyGlyGlyGluGluSerThrVal----- 726
 QY 452 ACCTTTATAGGTTTCTTCGTATCTTTTATTGCTCTCTGGAGTTCGTAATACTACC 511
 DB ----- 727
 QY 512 GGCAAGGACCGGTAGCTGCTCTACGGGTAGCTTGGATTGACAAAATGTCAGTTG 571
 DB ----- 733 GlyGlyGlyAlaLeu---LeuSerThrAsnGluValAsnValCysSerAsnGlnAsnVal 751

QY 572 CTCTTCAGCAAAACATTTTCAACG-----GATAATGGCGTGTCTATCACCAGAAA 622
 DB ValPheSerAspAsnValThrSerAsnGlyCysAspSerGlyAlaIleLeuAlaLys 771
 QY 623 ACTCTTTTATTAAAGGACTACAAATGTTCAGTCTCTGTTTCTGAAATATCTCTCAAG 682
 DB LysValAspIleSer---AlaAsnHisSerValGluPheValSerAsnGlySerGlyLys 790
 QY 683 AAAGCGGAGCCATT---CAGACTTCGATGCCCTTACCTACTGGAACCAAGGGGAA 739
 DB PheGlyGlyAlaValCysAlaLeuAsnGluSerValAsnIleThrAspAsnGlySerAla 810
 QY 740 GTCTCTTTTCTGACATATCTCTCGGATTCGGAGCTCGCAATTTTACA---GAAGCC 796
 DB ValSerPheSerLysAsnArgThrArgLeuGlyGlyAlaGlyValAlaAlaProGlnGly 830
 QY 797 TCGGTGACTATT---TCTAATAATGTAAAGTTTCTCTTATTGACATAAGGTACACAGGA 853
 DB SerValThrIleCysGlyAsnGlnGlyAsnIleAlaPheLysGluAsnPheValPheGly 850
 QY 854 GCGAGC----- 859
 DB SerGluAsnGlnArgSerGlyGlyAlaIleAlaAsnSerSerValAsnIleGln 870
 QY 860 -----TCCTCAACACGGGGATATGTCAGGA----- 886
 DB AspAsnAlaGlyAspIleLeuPheValSerAsnSerThrGlySerTyGlyGlyAlaIle 890
 QY 887 -----GGTGCTATCTGTATATAAAGTACAGATACATAGGTACACCTCACATGGA 940
 DB PheValGlySerLeuValAlaSerGluGlySerAsnProArgThrLeuThrIleThrGly 910
 QY 941 AATCAG---ANGTTACTCTTCAGCAACAATACATCGACAACAGCG----- 982
 DB AsnSerGlyAspIleLeuPheAlaLysAsnSerThrGlnThrAlaAlaSerLeuSerGlu 930
 QY 983 -----GGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGGCT-----TCC 1021
 DB LysAspSerPheGlyGlyGlyAlaIleTyThrGlnAsnLeuLysIleValLysAsnAla 950
 QY 1022 GGAGGACTTACCTTATTCAGTAGAATAATAGTGTCAATGAGGTACAGCTCTCTAAAGGTGGA 1081
 DB GlyAsnValSerPheTyR-----GlyAsnArgAlaProSerGlyAla 964
 QY 1082 GCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCCGCCGATAGTGTGACATTGTC 1141
 DB GlyValGlnIleAlaAspGlyGlyThrValCysLeuGluAlaPheGlyGlyAspIleLeu 984
 QY 1142 TTTTATAGGATACAGTCACCTTCTACTCTCTGGAGCAATAGTAGTAGTATCGACTTA 1201
 DB PheGluGlyAsnIle-----AsnPheAspGlySerPheAsnAlaIleHisLeuCys 1001
 QY 1202 GGAACGAGTGCAGAGATGACAGCTTTGCGTTCTGCTGTGAGAGCATCTACTCTTAT 1261
 DB GlyAsnAspSerLysIleValGluLeuSerAlaValGlnAspLysAsnIleIlePheGln 1021
 QY 1262 GATCCCATACATCAGGATCATCCACA-----ACAGTTACAGTGTCT----- 1303
 DB AspAlaIleThrTyGluGluAsnThrIleArgGlyLeuProAspLysAspValSerPro 1041
 QY 1304 -----TTAAAAGTTAATGACAGCTCCGGCA---GATTCTGCACACTACATAT 1345
 DB LeuSerAlaProSerLeuIlePheAsnSerLysProGlnAspAspSerAlaGlnHisHis 1061
 QY 1346 ACAGGCAACATCATCTTCACAGGAGAAAAGTTATCAGACAGAGCGCGCAGATTCTAAA 1405
 DB GluGlyThrIleArgPheSer----- 1068
 QY 1406 AATCTTACTTCGAAAGCTACTACGCTGTAACTCTTTTCAGGAGGTACTCTTATCTTTAAA 1465
 DB ArgGlyValSerLysIleProGlnIleAlaAlaIleGlnGluGlyThrLeuAlaLeuSer 1088

Qy	2333	CTTAGCTACACCCATACGGATACGATCTGTAAACCAAGTAT-----ACAACATAT	2383
Db	785	AlaAalatyGlytyrSerIysAsnHisLeuAsnThrThrTyLeuArgProAspLysAla	804
Qy	2384	CCTACTGTTAAAGACGCTGGGGAAATGATAGTTTCGCTTTTGAATTCGGTGGAAAGCT	2443
Db	805	ProLysSerGlnGlyGlnTrpHisAsnAsnSerTyTyTyValLeuIleSerAlaGluHis	824
Qy	2444	CCGATT-----TGCCTTAGATGAAGTGCCTCTATTTCAGCAGCTAC-----ATGCCC	2488
Db	825	ProPheLeuAsnTrpCysLeuLeuThrArgProLeuAlaGlnAlaTrpAspLeuSerGly	844
Qy	2489	TTCAATGAATTCGAGTTTGTCTATGCATCATCAGGAGGTTTAAAGAACAGGAAACAGAA	2548
Db	845	PheIleSerAlaGluPheLeuGlyGlyTrpGlnSerIysPheThrGluThrGlyAspLeu	864
Qy	2549	GCTCGTGAATTTGGAACTAGCCGCTTGTGAATCTTTCCTTACTATCGGGATCCGA---	2605
Db	865	GlnArgSerPheSerArgGlyIysGlyTyArgAsnValSerLeuProIleGlyCysSerSer	884
Qy	2606	-----TTTGATATAGGAATCATCAGCTGCCAAGATCCACAGTCAACATCTAACT	2650
Db	885	GlnTrpPheThrProPheLysLys-----AlaProSerThrLeuThrIleLys	900
Qy	2651	CTTGGTTATACTGTGGATCTTGTTCTGTAGTAAACCCGACTGTAGGACAACTGCCGAT	2710
Db	901	LeuAlaTyIysProAspIleTyArgValAsnProHisAsnIleValThrValValSer	920
Qy	2711	AGCGGTGATCTTGGAAAACTTCGGTACGAATTTGGCAAGACTTTAGTCTTCCTCGT	2770
Db	921	AsnGlnGluSerThrSerIleSerGlyAlaAsnLeuArgArgHisGlyLeuPheValGln	940
Qy	2771	GCAGGGACCAATTTTGTCTTAACTCAAAATTTGAAGCCCTTTAGCCAAATTTTCTTTGAA	2830
Db	941	IleHisaspValValAspLeuThrGluaspThrGlnAlaPheLeuAsnTyThrPheasp	960
Qy	2831	TTGCGTGGGTCACTCCGCAATTCATAGTGTAGACTTAGGACAAATACCAATTC	2884
Db	961	GlyIysAsnGlyPheThrAsnHisArgValSerThrGlyLeuLysSerThrPhe	978

Search completed: December 16, 2003, 10:24:11
Job time : 113.5 secs

QY	1397	GATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGGTACTCTA	1456
Db	461	LeuProAlaAsnThrThrThrIleuLeuGlyThrValIysIleAlaSerGlyGluLeu	480
QY	1457	TCTTTAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGCAGATTCGT	1516
Db	481	LysIleThrAspAsnAlaValValAsnValLeuGlyPheAlaThrGlnGlySerGlyGln	500
QY	1517	CTCGAAATCGAGCGTAGGAATACTCTA-----GAACCTCGTGAT	1555
Db	501	LeuThrLeuGlySerGlyGlyThrLeuGlyIleuAlaThrProThrGlyAlaProAlaAla	520
QY	1556	ACTAGC--ACCATCAACAATTTGGTCATTAACTCAGTCTTATAGACGGTGCACGAAG	1612
Db	521	ValAspPheThrIleGlyIysIleuAlaPheAspProPheSerPheLeuLysArgAspPhe	540
QY	1613	GCAAAAATAGAACCAACACTAGTCGTAATAAATCTGACTTTATCTGGAACCATCATTTA	1672
Db	541	ValSerAlaSerValAsnAlaGlyThrLysAsnValThrLeuThrGlyAlaLeuValLeu	560
QY	1673	TTGCACCCGCGGCAGC--TTTATGAAATCATAGTTTAAGAAATCCTCAGCTCTAC	1729
Db	561	AspGluHisAspValThrAspLeuTyArgMetValSerLeuGlnIleSerProValAlaIle	580
QY	1730	GACATCTTAGAGCTCAAAAGCTCTCGAACTGTAAACAGCACGCGAGTGACTCCAGATCCT	1789
Db	581	ProIleAlaValPheLysGlyAla--ThrValThrLysThrGlyPhe--ProAspGly	598
QY	1790	ATAATGGGTGAGAAATTCATTACGGCTATCAGGNACTGG-----	1831
Db	599	GluIleAlaThrProSerHisIstyGlyTyArgGlnGlyIstySerTyThrTrpSerArg	618
QY	1832	-----GGCCCA-----	1837
Db	619	ProLeuLeuIleProAlaProAspGlyGlyPheProGlyGlyProSerProSerAlaAsn	638
QY	1838	-----ATTGTTGGGGCAGGGCGCTTACGACTGCAACCTTCACTGGACTAA	1888
Db	639	ThrLeuTyAlaValTrpAsnSerAspThrLeuValArgSerThr-----	653
QY	1889	ACTGGCTATTCTCTAATCCGAGCGTATCGGCTCTTTAGTCCTCTAATAGCTTATGG	1945
Db	654	-----TyrIleLeuAspProGluArgTyGlyGluIleValSerAsnSerLeuThrIle	671
QY	1946	-----AATGCATTATAGATATTAGCTCTCTCCATTATCTTATGGAGACT	1990
Db	672	SerPheLeuGlyAsnGlnAlaPheSerAspIle-----LeuGlnAspValLeuLeuIle	689
QY	1991	GCAACAGNAGGTTGCGAGGAGCCGTCTTTTGGTGTGCTGGATTATCACTTCTTC	2050
Db	690	AspHisProGlyLeu-----SerIleThrAlaLysAlaLeuGlyAlaTyVal	705
QY	2051	CATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTTGAGTCGGGTATGTCATA	2110
Db	706	GluHisThrProArgGlnGlyHisGluGlyPheSerGlyArgTyGlyGlyTyArgAla	725
QY	2111	CGAGGAACCTACATCTTGTTCAGATAAGATTCTTAGCTGCTGATTTTGTGACTCTTT	2170
Db	726	AlaLeuSerMetAsnTyThrAspHisThrThrLeuGlyLeuSerPheGlyGlnLeuTy	745
QY	2171	GGAGAGATAGAGACTCTTTGTAGCTAAGAAATCAAGGTACAGTCTACGGAGAACTCTC	2230
Db	746	GlyLysThr-----	748
QY	2231	TATTACGACCAACAAACCTATATCTCTCTCTTGCAACTACGGCCTTGTTCGTG	2290
Db	749	-----AsnAlaAsnProTyArgSerArgCysSerGluGlnMetTyLeuLeu	764
QY	2291	TCTTAT-----GTTCTCTACAGATTCTGTCTCTTTTCAGGAAC	2332
Db	765	SerPhePheGlyGlnPheProIleValThrGlnLysSerGluAlaLeuIleSerTrpLys	784

DR Pfam: PF03797; Autotransporter; 1.
 DR Pfam: PF02415; DUF145; 1.
 DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs: TIGR01376; POMP_repeat; 6.
 SQ SEQUENCE 772 AA; 82931 MW; 484FC56D35801EB CRC64;

Alignment Scores:
 Pred. No.: 2,73e-226 Length: 772
 Score: 3991.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.87% Mismatches: 0
 Query Match: 73.78% Indels: 0
 DB: 16 Gaps: 0

US-09-428-122-1 (1-3000) x Q9RB71 (1-772)

QY	569	TTGCTCTTCAGAAAAA	CTTTTCAACGATATATGGCGTGCTATCACCGCAAAACTCTT	628
Db	1	MetLeuPheSerLysAsnPheSerThrAspAsnGlyGlyAlaIleThrAlaLysThrLeu	20	
QY	629	TCATTAAACAGGACTACAAATGTCAGCTCTGTTTCTGAAATAACCTCTCAAAAGAAAGGC	688	
Db	21	SerLeuThrGlyThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLysLysGly	40	
QY	689	GGAGCCATTACAGACTCCGATCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTT	748	
Db	41	GlyAlaIleGlnThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyGluValSerPhe	60	
QY	749	TCAGCAATACTCTTCGAGTTCGGAGCTGCAATTTTACAGAGCCCTCGGTGACTATT	808	
Db	61	SerAspAsnThrSerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIle	80	
QY	809	TCATAAATGCTAAAGTTCCTTTATTGACAATAAGGTACAGGAGCGAGCTCTCAACA	868	
Db	81	SerAsnAsnAlaLysValSerPheIleAspAsnLysValThrGlyAlaSerSerThr	100	
QY	869	ACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATCAAGTTC	928	
Db	101	ThrGlyAspMetSerGlyGlyAlaIleCysAlaIleLysThrSerThrAspThrLysVal	120	
QY	929	ACCTCAGTGGAAATCAGATGTTACTCTTCAGCAACAATACATCCGACACAGCGGAGGA	988	
Db	121	ThrLeuThrGlyAsnGlnMetLeuLeuPheSerAsnAsnThrSerThrAlaGlyGly	140	
QY	989	GCTATCTATGTGAAAGCTCGAAGTGGCTTCGGAGGACTTACCCCTATTTCAGTAGAAAT	1048	
Db	141	AlaIleThrValLysLysLeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerArgAsn	160	
QY	1049	AGTGTCAATGGAGGTACAGTCTCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAA	1108	
Db	161	SerValAsnGlyGlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGlu	180	
QY	1109	TTGAGTTATCCCGCATAGTGTGATGCTCTTTTGGGAATACAGTCACTTCTACT	1168	
Db	181	LeuSerLeuSerAlaAspSerGlyAspIleValPheLeuGlyAsnThrValThrSerThr	200	
QY	1169	ACTCTCTGGGACGAATAGAAGTAGTATCGACTTAGGAACGAGTCAAAAGATGACAGCTTTG	1228	
Db	201	ThrProGlyThrAsnArgSerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeu	220	
QY	1229	CGTTCTGCTCGGTAGAGCCATCTCTTCTATGATCCCATACTACAGATCATCCACA	1288	
Db	221	ArgSerAlaAlaGlyArgAlaIleThrPheThrAspProIleThrThrGlySerSerThr	240	
QY	1289	ACAGTTACAGATGCTTTAAAGTTAATGAGCTCCCGCAGATTCGCTACATATACA	1348	
Db	241	ThrValThrAspValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnThr	260	
QY	1349	GGGAACATCATCTTCACAGGAGAAAGTTATCAGACAGAGCGCGCAGATTTCTAAAAAT	1408	
Db	261	GlyAsnIleIlePheThrGlyGlyLysLeuSerGluThrGluAlaAlaAspSerLysAsn	280	
QY	1409	CTTACTTCGAAGCTTACTACAGCCCTGTAACTCTTTTCAGGAGGTACTCTATTCTTAAACAT	1468	

Db	281	LeuThrSerLysLeuLeuGlnProValThrLeuSerGlyGlyThrLeuSerLeuLysHis	300
QY	1469	GGAGTGAATCTGCAGACTCAGGCATTCACACAGCAGACATTCGCTCGAAATCGAC	1528
Db	301	GlyValThrLeuGlnThrGlnAlaPheThrGlnGlnAlaAspSerArgLeuGluMetAsp	320
QY	1529	GTAGGAATCTACTAGAACCTCTGATACCTAGACACCAATAACAATTTGGTCATTAAATC	1588
Db	321	ValGlyThrThrLeuGluProAlaAspThrSerThrIleAsnAsnLeuValIleAsnIle	340
QY	1589	AGTTCTATAGCGGTGCAAGAGGCAAAATAGAAACCAAGCTAGCTCAAAAATCTG	1648
Db	341	SerSerIleAspGlyAlaLysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeu	360
QY	1649	ACTTTATCTGGAACCATCCTCTTATTCGACCCGACGGCGACGTTTATGAAATCATAGT	1708
Db	361	ThrLeuSerGlyThrIleThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSer	380
QY	1709	TTAAGAAATCTCAGTCTCTAGCAGCATCTTAGAGCTCAAGCTTCTGGAACCTGTAACAGC	1768
Db	381	LeuArgAsnProGlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSer	400
QY	1769	ACCGCAGTGACTCCAGATCCTTATATGGTGAGAAATTCACATTACGGCTATCAGGGAAT	1828
Db	401	ThrAlaValThrProAspProIleMetGlyGluLysPheHisTyrGlyTyrGlnGlyThr	420
QY	1829	TGGGGCCCAATGTTTGGGGACAGGGGCTTCTACAGCTGCAACCTTCAACTGACATAA	1888
Db	421	TrpGlyProIleValTrpGlyThrGlyAlaSerThrThrAlaThrPheAsnTyrThrLys	440
QY	1889	ACTGGCTATATCTTAATCCCGAGGATCCGCTCTTTAGTCCCTTAATAGCTTATGGAT	1948
Db	441	ThrGlyTyrIleProAsnProGluArgIleGlySerLeuValProAsnSerLeuTrpAsn	460
QY	1949	GCATTATAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAACCAAGGTTGCAG	2008
Db	461	AlaPheIleAspIleSerSerLeuHisTyrLeuMetGluThrAlaAsnGluGlyLeuGln	480
QY	2009	GGAGACCGTGTCTTTTGGTGTCTGGATTCTAACTTCTTCCATPAAGATAGTACAAA	2068
Db	481	GlyAspArgAlaPheTrpCysAlaGlyLeuSerAsnPhePheHisLysAspSerThrLys	500
QY	2069	ACACACGGGGTTTCGCCATTTGAGTGGCGGTATGTCATAGGAGGAAACCTACATCT	2128
Db	501	ThrArgArgGlyPheArgHisLeuSerGlyGlyTyrValIleGlyGlyAsnLeuHisThr	520
QY	2129	TGCTTCAGATAAGATTCCTAGTCTCATTTTGTCTCAGCTCTTTTGGAGAGATAGAGACTAC	2188
Db	521	CysSerAspLysIleLeuSerAlaAlaPheCysGlnLeuPheGlyArgAspArgAspTyr	540
QY	2189	TTTGTAGCTAAGAAATCAAGGTACAGTCTACGGAGGAATCTCTATTACCAGACACAGAA	2248
Db	541	PheValAlaLysAsnGlnGlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisAsnGlu	560
QY	2249	ACCTATATCTCTTCTTCCTGCAACTACGGCTTGTCTGCTCTTATGCTTCTCCTACAGAG	2308
Db	561	ThrTyrIleSerLeuProCysLysLeuArgProCysSerLeuSerTyrValProThrGlu	580
QY	2309	ATTCTCTGTCTCTTTTCAGAAACCTTAGCTACCCATACCGATAACCATCTGAAAAAC	2368
Db	581	IleProValLeuPheSerGlyAsnLeuSerTyrThrHisThrAspAsnAspLeuLysThr	600
QY	2369	AAAGTATACAACTATCTACTCTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAA	2428
Db	601	LysTyrThrThrTyrProThrValLysGlySerTrpGlyAsnAspSerPheAlaLeuGlu	620
QY	2429	TTCCGTGGAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTTCAGCAGCTACATGCC	2488
Db	621	PheGlyGlyArgAlaProIleCysLeuAspGluSerAlaLeuPheGluGlnTyrMetPro	640
QY	2489	TTTCATGAATTCAGTTTCTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAA	2548

Db 641 PheMetLysLeuGlnPheValTyAlaHisGlnGluGlyPheLysGluGlnGlyThrGlu 660
 Qy 2549 GCTGCTGAATTTGGAAGTAGCGCTTGTGTAATCTTGCTTACCTATCGGATCCGATTT 2608
 Db 661 AlaArgGluPheGlySerArgLeuValAsnLeuAlaLeuProIleGlyLeuArgPhe 680
 Qy 2609 GATAAGGATCAGACTGCGCAGAGTCAAGTACATCTAACTCTGGTATCTGCTGAT 2668
 Db 681 AspLysGluSerAspCysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValAsp 700
 Qy 2669 CTGTGCTGTAGTAACCCGACTGTACGACACACACTAGCGGTGATCTTGGAAA 2728
 Db 701 LeuValArgSerAsnProAspCysThrThrThrLeuArgIleSerGlyAspSerTrpLys 720
 Qy 2729 ACCTTCGGTAGCAATTTGGCAAGCAAGCTTTAGTCTTCGTGCGAGGAAACATTTTGC 2788
 Db 721 ThrPheGlyThrAsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCys 740
 Qy 2789 TTTAACTCAAAATTTGAAGCTTTAGCCATTTTTCGTAATTCGGTGGTCACTCTCGC 2848
 Db 741 PheAsnSerAsnPheGluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArg 760
 Qy 2849 AATTACAATGTAGCTTAGGACCAAAATACCAATTC 2884
 Db 761 AsnTyrAsnValAspLeuGlyAlaLysTyrGlnPhe 772

RESULT 2
 P71135
 ID P71135 PRELIMINARY; PRT; 926 AA.
 AC P71135;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative 98 kDa outer membrane protein.
 OS Chlamydomophila abortus.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
 OX NCBI_TaxID=83555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ovine abortion S26/3;
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
 RT "98kDa protein genes from ovine abortion strain S26/3 Chlamydia
 RT psittaci";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; J72499; AB18188.1; -;
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; DUF145; 2.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 SQ SEQUENCE 926 AA; 98439 MW; 3E755E2F594750F CRC64;

Alignment Scores:

Pred. No.: 1.86e-104 Length: 926
 Score: 1915.00 Matches: 410
 Percent Similarity: 59.27% Conservative: 156
 Best Local Similarity: 42.93% Mismatches: 333
 Query Match: 35.40% Indels: 56
 Gaps: 2

US-09-428-122-1 (1-3000) x P71135 (1-926)

Qy 101 ATGAGTCTCTTCCCAAGTTGTGATTTTCTACATTTGCTATTTTCCCTTTGTCTATG 160
 Db 1 MetArgProSerLeuTyrLysIleLeuIleSerSerThrLeuThrLeuProIleSerPhe 20
 Qy 161 -----ATTGCTACCGAGACAGATTTTGGATTCAGT 190
 Db 21 HisPheSerGlnLeuHisAlaGluValAlaLeuThrGlnGluSerIleLeuAspAla--- 39
 Qy 191 GCGAGTTTCGATGGGAATAAAATGTAATTTTTCAGTTCGTGAGAGTCAAGAGATGCT 250

Db 40 -----AsnGlyAlaPheSerProGlnSerThrSerThrAlaGly 52
 Qy 251 GGAATCTACCTATTTAAAGGAAATGTCACTCTAGAAAATATTTCTCGAACAGGACACA 310
 Db 53 GlyThrIleTyrAsnValGluSerAspIleSerIleValAspVal---GlyGlnThrAla 71
 Qy 311 GCATCACAAAAAGCTGTTTAAACAACACTAAGGCGCATTTGACTTTTCACAGGTAAACGG 370
 Db 72 AlaLeuAlaSerSerAlaPheValGlnThrAlaAspAsnLeuThrPheLysGlyAsnAsn 91
 Qy 371 AACTCTCTATTGTTCCAAAACGTCGATGTCAGGAGCTGTAGCAGGCGTCTGTTTAAACAGC 430
 Db 92 HisSerLeuSerIleThrAsnAlaAsnAlaGly---AlaAsnProAlaGlyIleAsnVal 110
 Qy 431 AGCGTGTAGATAAATCTACACCGTTTTATAGGGTTTTCTTCGCTATCTTTTATTCGCTCT 490
 Db 111 AsnThrAlaAspLysIleLeuThrLeuThrAspPheSerLysLeuSerPheLysGluCys 130
 Qy 491 CCTGGAAGTTCGATAACTACCGGCAAGAGCCCTGTAGCTCTCTACGGGTAGCTTGAGT 550
 Db 131 ProSerSerLeuValAsnThrGlyLysGlyAlaMetLys---SerGlyGlyAlaLeuAsn 149
 Qy 551 TTGACAAAATAATGTCACTCTCTCAGCAAAAACCTTTTCAACGGATAATGGCGGTGCT 610
 Db 150 LeuAlaAsnAsnAlaSerIleLeuPheAspGlnAsnTyrSerAlaGluAsnGlyGlyAla 169
 Qy 611 ATCAGCGCAAAAACCTCTTTTCAACAGGGGACTACAATGTGAGCTCTGTTTCTGAAAAT 670
 Db 170 IleSerCysLysAlaPheSerLeuThrGlySerSerLysGluIleSerPheThrThrAsn 189
 Qy 671 ACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTTACTGGAAC 730
 Db 190 SerThrAlaLysLysGlyGlyAlaIleAlaThrGlyIleAlaHisLeuSerAspAsn 209
 Qy 731 CAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTTCTGGAGCTGCAATTTTACA 790
 Db 210 GlnGlyThrIleArgPheSerGlyAsnThrAlaValAsnSerGlyGlyAlaValTyrSer 229
 Qy 791 GAAGCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTTATTTGACAATAAGTCA 850
 Db 230 GluAlaSerMetThrIleAlaGlyAsnAsnHisValAlaPheSerAsnAsnAlaValSer 249
 Qy 851 GGAGGAGCTCTCTCAACACCGGGGATGTCTCAGGAGGTGCTATCTGTCTTATAAACT 910
 Db 250 GlySerSer-----AspGlyCysGlyGlyAlaIleHisCysSerLysThr 264
 Qy 911 AGTACAGATATAAGTCACTGGAATCAGATGTTACTCTTCAGCAACAATACA 970
 Db 265 GlySerAlaProThrLeuThrIleArgAspAsnLysValLeuIlePheGluGluAsnThr 284
 Qy 971 TCGAACACGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGTGGCTTCGAGAGACTT 1030
 Db 285 SerSerAlaLysGlyGlyAlaIleTyrThrAspLysLeuIleLeuThrSerGlyGlyPro 304
 Qy 1031 ACCCTATTTCAGTAGAATAGTGTCAATCGAGGTACAGCTCTCTAAGTGGGCGCCATAGCT 1090
 Db 305 ThrAlaPheIleAsnAsnLysValThrHisAlaThr---ProLysGlyGlyAlaIleGly 323
 Qy 1091 ATCGAAGATAGTGGGGAATTCAGTTTATCCCGCATAGTGGTGACATTTCTTTTAGGG 1150
 Db 324 IleAlaAlaAsnGlyGluCysSerLeuThrAlaGluHisGlyAspIleThrPheAspAsn 343
 Qy 1151 AATACAGTCACTCTTACTACTCTCTGGGAGC---AATAGAGTAGTATCATCTTAGGAACG 1207
 Db 344 AsnLeuMetAlaThrGlnAspAsnAlaThrIleLysArgAsnAlaIleAsnIleGluGly 363
 Qy 1208 AGTCAAGATGACAGCTTTGGTCTCTGCTGTAGAGCATCTTCTATCTATCATCC 1267
 Db 364 AsnGlyLysPheValAsnLeuArgAlaAlaSerGlyLysThrIleSerPheTyrAspPro 383
 Qy 1268 ATAACCTACAGGATCATCCACACAGTTTACAGATGCTTAAAGTGTAAATGAGACTCCGCA 1327

Percent Similarity:	54.17%	Conservative:	136
Best Local Similarity:	40.00%	Mismatches:	287
Query Match:	30.68%	Indels:	153
DB:	2	Gaps:	25

US-09-428-122-1 (1-3000) x P77792 (1-839)

Qy	89	ATATATTTTCAATGAAGTCTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTTC	148
Db	5	ValTyrTrpPheLeuIleSerSer-----SerLeupheAlaSerAsn	18
Qy	149	CTTTGCTATGATT---GCTACCGACAGATTTTGGATCAAGTCGAGTTTCGATGG	205
Db	19	SerLeuSerPheAlaAsnAspAlaGlnThrAlaLeuThrProSerAspSerTyrAsnGly	38
Qy	206	AAT---AAAAATGCTAATTTTTCAGTTTCGTGAGAGTCAGGAAGATGCTGAACTACTAC	262
Db	39	AsnValThrSerGluGluPheGlnValGlySerGluThr-----SerSerGlyThrThrTyr	56
Qy	263	CTATTTAAGGGAATGTCACTCTAGAAAATATTTCTTGGAAACAGCGACAGCAATCAAAA	322
Db	57	ThrCysGluGlyAsnValCysIle---SerPheAlaGlyLysAspSerGlyLeuLysLys	75
Qy	323	AGCTGTTTTAACACACTAAGGGCGATTTGACITTTACAGGTAACGGGAACCTCTATTG	382
Db	76	SerCysPheSerAlaThr---AspAsnLeuThrPheLeuGlyAsnGlyTyrThrLeuCys	94
Qy	383	TTCCAAACGGTGGATGCAAGGACTGTAGCAGGGGCTGCTGTTAAACAGCAGCGTGGTAGAT	442
Db	95	PheAspAsnIleThrThrAlaSerAsnProGlyAlaIleAsnValGlnGlyGlnGly	114
Qy	443	AAATCTACACGTTTATAGGGTTTTCTTCGCTATCTTTTATATGCGTCTCTCGAAGTTCG	502
Db	115	LysThrLeuGlyIleSerGlyPheSerLeuPheSerCysAlaTyrCysProGly---	133
Qy	503	ATACTACCGCAAGAGCGGTAGCTGCTCTACGGGTAGCTTGAGTTGATTCACAAAAT	562
Db	134	---ThrThrGlyTyrGlyAlaIleGln---ThrLysGlyAsnThrThrLeuLysAspAsn	151
Qy	563	GTCAGTTTGCCTTCAGCAAAAACCTTTTCAACGGATAATGCGGTGCTATCACGCCAAA	622
Db	152	SerSerLeuValPheHisLysAsnCysSerThrAlaGluGlyGlyAlaIleGlnCys---	170
Qy	623	ACTCTTTTCAATTAAACAGGGACTACAATGTCACTCTGTTTTCTGAAAATACCTCTCAAAG	682
Db	170	-----	170
Qy	683	AAAGCGGAGGCATTCAGACTTCGATGCGCTTACCATTACTGAAACCAAGGGGAAGTC	742
Db	170	-----	170
Qy	743	TCTTTTCTGCAATACTTCTTCGGATTCCTGGAGTCTGCAATTTTTCACAGAGCCTCGGTG	802
Db	170	-----	170
Qy	803	ACTATTTCTAATTAATGCTAAAGTTTTCCTTTATTGACAATAAGTTCACAGGCGAGCTCC	862
Db	170	-----	170
Qy	863	TCAACAACGGGGATATGTCAGGAGTCTATCTGTGCTTATAAACTAGTACAGATACT	922
Db	171	-----LysGlySerSerAspAla	176
Qy	923	AAGGTCACCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACACACGCG	982
Db	177	GluLeuLysIleGluAsnAsnGlnAsnLeuValPheSerGluAsnSerSerThrSerLys	196
Qy	983	GGAGGAGCTATCTATGTGAAAAGCTCCGAACCTGGCTCCCGAGGACATTCACCTATTCA	1042
Db	197	GlyGlyAlaIleTyrAlaAspLysLeuThrIleValSerGlyGlyProThrLeuPheSer	216
Qy	1043	AGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGCCATGCTATCGAAGAT---	1099

QY 809 TCTAATAATGCTAAAGTTTCCTTTATTCACAATAAGGTCACAGGAGCGAGCTCCTCAACA 868
Db |||
186 GluAsn----- 187
QY 869 ACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACAGGTC 928
Db |||
187 ----- 187
QY 929 ACCCTACTGGAAATFCAGATGTTACTCTTCAGCAA CAATACATCGACAACAGCGGAGGA 988
Db |||
188 -----AsnGlnAsnLeuValPheAlaGluAsnSerSerSerSerGlyGly 203
QY 989 GCTATCTATGCAAAAAGCTGGAACCTGCTCCGAGGAGCACTTACCTATTTCAGTAGAAT 1048
Db |||
204 AlaIleTyrAlaAspLeuThrIleValSerGlyGlyProThrLeuPheSerAsnAsn 223
QY 1049 AGTGTCAATGGAGGTACAGCTCCTAAAGGTGAGCATAGCTATCGAAGATAGT---GGG 1105
Db |||
224 SerValSer---AlaSerSerProLysGlyAlaIleCysIleLysAspSerGlyGly 242
QY 1106 GAATTGAGTTATCCCGCATAGTGGTGCATGTCTTTTGGGAATACAGTACTTCT 1165
Db |||
243 GluCysSerLeuThrAlaAspLeuGlyAspIleThrPheAspGlyAsnLysIleLys 262
QY 1166 ACT-----ACTCTGGGACGATAGAGTAGTATCGACTTAGGACGAGTCAAG 1216
Db |||
263 ThrAsnGlyGlySerProThrValThrArgAsnSerIleAspLeuGlySerSerGlyLys 282
QY 1217 ATGACAGCTTTCGTTCTGCTCTGCTAGAGCCATCTACTCTATGATCCCACTATACA 1276
Db |||
283 PheThrLysLeuAsnAlaGlyGluPheGlyPheGlyIlePhePheTyrAspProIleThrGly 302
QY 1277 GGATCATCCACAACAGTTACAGATGTCTTAAAGTTAAATGAGACTCCGGCAGATTCTGCA 1336
Db |||
303 GlyGlySer-----AspGluLeuAsnIleAsnLys-----GlnAspThr 315
QY 1337 CTACATATACAGGNACTCATCTCTCACAGAGAAAGTTATTCAGACAGAGCCGCA 1396
Db |||
316 ValAspTyrThrGlyLysIleValPheSerGlyGluArgLeuSerAspGluGlyLys 335
QY 1397 GATTCTAAAATCTTACTTCGAAGCTACTACAGCTGTAACTCTTTCAGGAGTACTCTA 1456
Db |||
336 ValAlaAlaAsnLeuLysSerAspPheLysGlnProLeuLysIleGlySerGlySerLeu 355
QY 1457 TCTTTAAAACATGGAGTACTCTGCAGACTCGGCATTCACCAACAGCAGACTTCGT 1516
Db |||
356 IleLeuLysAspGlyValThrLeuGluThrLysSerPheThrGlnThrGluGlyAlaThr 375
QY 1517 CTCGAAATGGAGTAGGAATCTACTAGAACCT-----GCTGATACTAGCACC 1564
Db |||
376 ValValMetAspLeuGlyThrThrLeuGlnThrProSerSerGlyGlyGluThrIleThr 395
QY 1565 ATAAACAATTTGCTCATTAAACATCAGTTCTATAGACGGTGCA-----AAGAAG 1612
Db |||
396 LeuThrAsnLeuAspIleAsnValAlaSerLeuGlyGlyGlyValAlaProAspPro 415
QY 1613 GCAAAAATAGAAACCAAGCTACGTCAAAATACTGACTTTTATCGGAACCATCTTFA 1672
Db |||
416 AlaLysValGluAlaThrThrGluSerLysThrValThrIleAsn---AlaValAsnLeu 434
QY 1673 TTGGACCGGACGGCGCTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTCAGCAG 1732
Db |||
435 ValAspAspAsnGlyAsnAlaTyrGluTyrProIleLeuAlaAlaSerGlnProPheThr 454
QY 1733 ACTTTAGAGCTCAAA-----GCTCTGGAACGTGTAAACAAGCAGCCAGTG----- 1777
Db |||
455 AlaIleGluValArgSerGlySerSerGlySerIleThrLysProThrThrAsnLeuGlu 474
QY 1778 -----ACTCCAGATCCTATAATGGTGAGAAATTCATTAGCGCTATCAGGGAACCTGG 1831
Db |||
475 AsnTyrThrProProThr-----HisTyrGlyTyrGlnGlyAsnTrp 488

1832 GGCCCAATTGTTGGGGACAGGGGCTTCTAGG-----ACTGCAACCTTCAACTGG 1882
Db ---ThrValThrTrpLysGlnGlySerSerAlaGlnGluLysThrAlaThrLeuThrTrp 507
QY 1883 ACTAAACTGGCTATATTCTTAATCCCGAGGATCGGCTCTTTAGTCCCTTAATAGCTTA 1942
Db |||
508 GluGlnThrGlyTyrSerProAsnProGluArgGlnGlySerLeuValProAsnThrLeu 527
QY 1943 TGGATGCAATTTATAGATATTAGTCTCTCTCATTTCTTATGGAGAGCTGCAAAAGAGG 2002
Db |||
528 TrpGlySerPheSerAspIleArgAlaIleGlnAsnLeuMetAspIleSerValAsnGly 547
QY 2003 TTGCAGGAGAGCGGCTTTTGTGTGCTGATTTATCTAACTTCTTCCATAAGGATAGT 2062
Db |||
548 AlaAspTyrHisArgGlyPheTrpValSerGlyLeuGlyAsnPheLeuHisLysSerGly 567
QY 2063 ACAAAAACACAGCGCGGTTTCGCCATTGTAGTGGCGGTATGTATAGGAGGAAACCTA 2122
Db |||
568 SerAspThrLysAsGlyPheArgHisAsnSerAlaGlyTyrAlaLeuGlyValTyrAla 587
QY 2123 CATACTTGTTCAGATAGATTCTTAGTCTGCATTTGTCTAGCTCTTTGGAGAGATAGA 2182
Db |||
588 GlnThrProSerGluAspValPheSerAlaAlaPheCysGlnLeuPheGlyLysAspLys 607
QY 2183 GACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGAGGAACTCTCTATTACCAGCAC 2242
Db |||
608 AspTyrLeuValSerLysAsnSerThrValTyrAlaGlySerIleTyrGlnHis 627
QY 2243 AACGAAACCTATATCTCTTCTTCTTGTGCAACTCGGCCCTTGTCTGTCTTATGTTCT 2302
Db |||
628 -----IleSerTyrTrpAsn 632
QY 2303 ACA-----GAGATTCTGTCTCTCTTTCAGGA 2329
Db |||
633 ThrTrpAsnThrLeuLeuGlnAsnThrLeuGlyAlaGluAlaProLeuValLeuAsnAla 652
QY 2330 AACTTACTACACCATACGATAACGATCTGAAACCAAGTAT----- 2374
Db |||
653 GlnLeuAlaTyrCysHisAlaSerAsnAsnMetLysThrAsnMetThrAspThrTyrAla 672
QY 2375 -----ACAACATATCTCTGTTTAAAGAGAGCTGGGGAAATGATAGTTTCCCTTTA 2425
Db |||
673 ProProLysThrThrTyrSerGluIleLysGlyAspTrpGlyAsnAspCysPheGlyVal 692
QY 2426 GAATTCGGTGAAGAGCTCCGATTTGCTTAGTAAAGTGTCTATTAGCAGCATACATG 2485
Db |||
693 GluPheGlyAlaLysAlaProIle---GluThrAlaSerLeuLeuPheAspMetTyrSer 711
QY 2486 CCTTCATGAATTCAGTTTGTCTATGCATCAGGAAGGTTTAAAGAACAGGGAACA 2545
Db |||
712 ProPheValLysLeuGlnLeuValHisAlaHisGlnAspAspPheLysGluAsnAsnSer 731
QY 2546 ---GAAAGCTCGTGAATTTGGAAGCGCTCTTGTGAATCTTGTGCTTACCTATCGGATC 2602
Db |||
732 AspGlnGlyArgTyrPheGluSerAsnAsnLeuThrAsnLeuSerMetProIleGlyVal 751
QY 2603 CGATTTGATAGGAATCAGATCGCAAGATCGAAGTCAATCTTAACCTCTGTTTACT 2662
Db |||
752 LysLeuGluLysPheSerHisLysAspThrAlaSerTyrAsnLeuThrLeuAlaTyrAla 771
QY 2663 GTGGATCTTGTTCGTAGTAACCCGACTGTAGCAACAACACTCGCAATTTAGCGGTGATCT 2722
Db |||
772 ProAspIleValArgSerAsnProAspCysThrAlaSerLeuLeuValSerProThrSer 791
QY 2723 -----TGAAGAACTTCGGTACCAATTTGGCAGACCAAGCTTTTGTCTCGTCAGGG 2776
Db |||
792 AlaValTrpValThrLysAlaAsnAsnLeuAlaArgHisAlaPheIleLeuGlnAlaGly 811
QY 2777 AACCAATTTTGTCTTAACCTCAAAATTTTGAAGCTTTAGCCATTTCTTTGAAATGGCT 2836
Db |||
812 AsnTyrLeuAlaLeuThrArgAsnThrGluLeuPheSerGlnPheGlyPheGluLeuArg 831
QY 2837 GGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCAATTC 2884

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Db      832 GlySerCysArgThrTyrAsnIleAspLeuGlySerLysIleGlnPhe 847
      ||||| ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 5
P71133 PRELIMINARY; PRT; 846 AA.
ID P71133;
AC P71133;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE POM91B precursor.
DE Chlamydia abortus.
OS Chlamydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83555;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RC STRAIN=96406378; PubMed=8810511;
RX Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins
of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the
highly immunogenic cluster of 90-kilodalton envelope proteins from the
Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
DR ENBL; U65943; AAC15923.1; -.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 846 POMP91B.
SQ SEQUENCE 846 AA; 90834 MW; 4CDC31DC03C2964E CRC64;

Alignment Scores:
Pred. No.: 2,87e-86 Length: 846
Score: 1605.00 Matches: 375
Percent Similarity: 53.02% Conservative: 143
Best Local Similarity: 38.38% Mismatches: 279
Query Match: 29.67% Indels: 180
DB: 2 Gaps: 28

US-09-428-122-1 (1-3000) x P71133 (1-846)
QY 89 ATATATTTTCAATGAAGTCTTCTTCCCAAGTTTGTATTTCTACATTTGCTATTTC 148
Db 5 ValTyrTrpPheLeuIleSerSer-----SerLeuLeuAlaSerAsn 18
QY 149 CCCTTGCTATGATT--GCTACCGACAGACAGTTTGGATTCAAGTGGAGTTTCGATGGG 205
Db 19 SerLeuSerPheAlaGlnValThrAsnGluThrLeuThrSerSerPheTyrAsnGly 38
QY 206 AAT---AAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACCTACCTAC 262
Db 39 AsnValThrSerAspGluPheGluValLysGluThr-----ThrSerGlyAlaIleTyr 56
QY 263 CTATTTAAGGAATGTCATCTAGAAAATATTCCTGGAAACAGCAGCAGCATCACAAA 322
Db 57 ThrCysGluGlyAsnValCysIle---SerTyrAlaGlyLysAspSerProLeuAsnLys 75
QY 323 AGCTGTTTTAACACACTAAGGGGATTTGCTTTTCAGGTACCGGAACCTCTCTATTG 382
Db 76 SerCysPheSerGluThrThrGluAsnLeuSerPheIleGlyAsnGlyTyrThrLeuCys 95
QY 383 TTCCAAACGGTGGATGCAGGACGTAGCAGGGGCTGTGTAAACAGCAGCGTGGTAGAT 442
Db 96 PheAspAsnIleThrThrGlnSerSerHisProGlyAlaIleSerValSerGlyThrAsn 115

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QY 443 AAATCTACCAGTTTATAGGGTTTCT-----TCGCTATCTTTTATTCGCTCTCTCGGA 496
Db 116 LysThrLeuAspIleSerGlyPheSerLeuPheSerCysAlaTyrCysCysProProGly 135
QY 497 AGTTCGATACTACCGCAAGAGAGCCGTTAGCTGCTCTACGGGTAGCTTGAGTTGTGACA 556
Db 136 -----ThrThrGlyTyrGlyAlaIleGln---ThrLysGlyThrThrLeuLys 151
QY 557 AAAAATGTCAGTTTGCTCTTCAAGAAAATCTTTCAACGGATAATGCGGGTGTCTATACC 616
Db 152 AspAsnSerSerLeuValPheHisLysAsnCysSerThrAlaGluGlyGlyAlaIleGln 171
QY 617 GCATAAACTCTTTCATTACACGGGACTACAATGTGAGCTCTGTTTCTGAAAATACCTCC 676
Db 172 CysLys----- 173
QY 677 TCATAAGAAAGCGGAGCCATTACAGACTTCCGATGCCCTTACCATTACTTGGAAACCAAGG 736
Db 173 ----- 173
QY 737 GAAGTCTCTTTTCTGCAATACACTTCTTCGGATTCTGGAGTCTGCAATTTTACAGAAGCC 796
Db 173 ----- 173
QY 797 TCGGTGACTATTCTTAATAATGCTAAAGTTTCTTTTATTGACATAAGTACAGTCACAGGCG 856
Db 173 ----- 173
QY 857 AGCTCTCTCAACAAACGGGGATATGTGACGAGGTGCTATCTGTGCTTATAAACTAGTACA 916
Db 174 SerSerSerSerThrAlaGluLys----- 182
QY 917 GATACTAAGTCACTCTACTCGGAATACAGATGTTACTCTTCAGCAACATACATCGACA 976
Db 183 -----LeuGluAsnAsnLysAsnLeuValPheSerGluAsnSerSerLys 197
QY 977 ACACGGGAGGAGCTATCTATGTGAAAAGCTCGAACTGCTTCCGAGGACTTACCCTTA 1036
Db 198 GluLysGlyGlyAlaIleTyrAlaAspLysLeuThrIleValSerGlyGlyProThrLeu 217
QY 1037 TTCAGTAGAATAGTGTCAATGGAGGTACAGCTCTCTAAAGTGGAGCCATAGCTATCGAA 1096
Db 218 PheSerAsnAsnSerValSerHisAsnSerSerProLysGlyGlyAlaIleCysIleLys 237
QY 1097 GATAGT---GGGAATTGAGTTTATCCGCGGATAGTGGTGGACATGCTCTTTTAGGAAT 1153
Db 238 AspSerAspGlyGluCysSerLeuThrAlaAsnLeuGlyAspIleThrPheAspGlyAsn 257
QY 1154 ACAGTCACTTCTACT-----ACTCTGGGACGAATAGAAAGTAGTAGTATCGACTTAGGA 1204
Db 258 LysIleIleThrThrAsnGlySerProThrValThrArgAsnSerIleAspLeuGly 277
QY 1205 ACAGGTGCAAGATGACAGCTTTGCTGCTGCTGGTGGTAGCCATCTACTCTATGAT 1264
Db 278 SerGlyGlyLysPheThrLysLeuAsnAlaLysGluGlyPheGlyIlePhePheTyrAsp 297
QY 1265 CCATA---ACTACAGATCATCCCAACAGITACAGATGCTCTTAAAGCTTAATGAGCT 1321
Db 298 ProIleAlaAsnThrGlySerThrGluIle-----GluLeuAsnLysThr 313
QY 1322 CCGGAGATTCTGCACATAATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCA 1381
Db 314 GluSerAspThrThr-----TyrThrGlyLysIleValPheSerGlyGlyLysLeuSer 331
QY 1382 GACACAGAGCCGACGATTCTAAAAATCTTACTTCGAAGCTACTACAGCTGTGAACCTT 1441
Db 332 AspGluGlyLysThrValProAlaAsnLeuLysSerTyrPheLysGlnProLeuLysIle 351
QY 1442 TCAGGAGGTACTCTATCTTTAAACATGAGTGAAGTCTCTCGAGACTCAGGCACTCACTCA 1501
Db 352 GlyAlaGlySerLeuValLeuLysAspGlyValThrLeuGluAlaLysIleThrGln 371

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QY 1502 CAGCAGATTCTCTCGTTCGAAATGAGCTAGGAACTACTCTAGAA-----CCT 1549
Db 372 ThrLysGlySerThrValValMetAspLeuGlyThrThrLeuGlnThrProSerSerSer 391
QY 1550 GCTGATCTAGCACCATAAACAATTTGGTCATTAAACATCAGTCTCTATA-----GAC 1600
Db 392 GlyGluThrIleThrLeuThrAsnLeuAspIleAsnIleAlaSerLeuGlyGlyGly 411
QY 1601 GGTCAAGAAGGCAAAATAGAACCAAGCTAGCTGCAAAATCTGACTTTATCTGGA 1660
Db 412 GlyThrAlaProAlaLysLeuAlaThrAsnThrAlaSerGlnAlaIleSerIleAla--- 430
QY 1661 ACCATCATTTATGACCGGACGGCAGGCTTTATGAATCATAGTTTAAAGAAATCCT 1720
Db 431 AlaValAsnLeuValAsnThrAspSerAsnThrTyrGluAspProIleLeuSerAlaSer 450
QY 1721 CAGTCTACGACATCTTAGAGCTCAAAAGCTTCTGGAAGCTGTAACAGCACGCGAGTACT 1780
Db 451 LysSerPheSerAlaIle-----ThrAlaThrThrSerSerSerThrValThr 466
QY 1781 CCAGATCTATAATGGGTGAGAAATTC-----CATTCGGCTATCAGGAACT 1828
Db 467 ProProGluThrAsnLeuLysAsnTyrThrProThrHisTyrGlyTyrGlnGlyAsn 486
QY 1829 TGGGGCCCAATTTGTTGGGGACAGGGGCTTCTACG-----ACTGCAACCTTCAAC 1879
Db 487 Trp---ThrValThrTrpLysGlnGlySerSerAlaGlnGluLysThrAlaThrLeuThr 505
QY 1880 TGGACTAAATCGGTATATTCTTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGC 1939
Db 506 TrpGluGlnThrGlyTyrSerProAsnProGluArgValGlySerLeuValProAsnThr 525
QY 1940 TTATGGAATGATTTATAGATTAATAGCTCTCTCCATTTATCTTATGAGACTGCAACGAA 1999
Db 526 LeuTrpGlyAlaPheSerAspThrArgAlaIleGlnAsnLeuMetAspIleSerValAsn 545
QY 2000 GGGTTGCAGGAGACCGGCTTTTGGTGTGCTGGATTATCTTAAGTCTTCCATAGGAT 2059
Db 546 GlyAlaAspTyrSerArgGlyPheTrpValSerSerLeuAlaAsnPheLeuAsnLysSer 565
QY 2060 AGTACAAAAACACGACGGGGTTTCGCCATTTAGTGGCGGTATGTCTAGGAGGAAC 2119
Db 566 GlySerAspThrLysArgLysPheArgHisHisSerAlaGlyTyrAlaLeuGlyValTyr 585
QY 2120 CTACATATTTGTTCAGATAAGATTTCTAGTGTGCTGATTTGTCAGCTTTTGGAGAGAT 2179
Db 586 AlaGlnThrProSerAspValCysSerAlaAlaPheCysGlnLeuPheGlyLysAsp 605
QY 2180 AGAGACTACTTTGTAGCTAAGATCAAGTACAGTACAGTACGGAGGAACTCTCTATTACCAG 2239
Db 606 LysAspTyrPheValSerLysAsnSerSerThrIleTyrAlaGlySerIleTyrTyrGln 625
QY 2240 CACAACGAAACCTATATCTCTCTCTGCAACTACGGCCTTGTTCGTGTCTTATGTT 2299
Db 626 His-----IleSerTyrTrp 630
QY 2300 CCTACA-----GAGATTCCTGTTCTCTTTCA 2326
Db 631 AsnThrTrpAsnThrLeuLeuGlnAsnThrLeuGlyAlaGluAlaProLeuValLeuAsn 650
QY 2327 GGAACCTTAGCTACACCCATCAGGATACGATCTCGAAACCAAGTATACA----- 2377
Db 651 AlaGlnLeuThrTyrCysHisAlaSerAsnMetLysThrAsnMetThrAsnThrTyr 670
QY 2378 -----ACATATCTACTGTTAAAGGAAGCTGGGGAATCATAGTTTCGCT 2422
Db 671 ThrProLysAsnValThrProSerGluIleLysGlyAspTrpGlyAsnAspCysPheGly 690
QY 2423 TTAGATTCGGTGAAGACTCCGATTTGCTTAGTGAAGAGTCTCTATTGACGAGTAC 2482
Db 691 ValGluPheGlyAlaLysAlaProIle---GluThrAlaSerLeuLeuPheAspMetTyr 709
QY 2483 ATGCCCTTCATGAATTCAGTTTGTCTATGCATCAGGAAGGTTTAAAGACGGGA 2542
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Db 710 SerProPheValLysLeuGlnLeuValHisAlaHisGlnAspAspPheLysGluAsnAsn 729
QY 2543 ACA---GAAGCTCGTGAATTTGGAAGTAGGCGGCTTGTGTAATCTTGCCTTACCTATCGGG 2599
Db 730 SerAspGlnGlyArgTyrPheGluSerAsnAsnLeuThrAsnLeuSerMetProIleGly 749
QY 2600 ATCCGATTTGATAGGAATCAGAGTGCACAGATGCAAGTACAACTTAACCTCTTGGTTAT 2659
Db 750 ValLysLeuGluLysPheSerHisLysAspThrAlaSerTyrAsnLeuThrLeuAlaTyr 769
QY 2660 ACTGTGATCTTGTTCGTAGTAAACCCGACTGTACGACAACTGCGAATTTAGCGGTGAT 2719
Db 770 AlaProAspIleValArgSerAsnProAspCysThrAlaSerLeuLeuValSerProThr 789
QY 2720 TCT-----TGGAAAACCTTCGGTACGAATTTGCAAGACAAAGCTTTAGCTTCGTGCA 2773
Db 790 SerAlaValTrpValThrLysAlaAsnAsnLeuAlaArgHisAlaPheIleLeuGlnAla 809
QY 2774 GGAACCATTTTTCGTTTAACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTGAATTG 2833
Db 810 GlyAsnTyrLeuAlaLeuThrArgAsnThrGluLeuPheSerGlnPheGlyPheGluLeu 829
QY 2834 CGTGGGTCTATCTCGCAATTTACAATGTAGACTTAGGAGCAAAATACCAATTC 2884
Db 830 ArgGlySerCysArgThrTyrAsnIleAspLeuGlySerLysIleGlnPhe 846

RESULT 6
Q8VU49 PRELIMINARY; PRT; 602 AA.
AC Q8VU49;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative polymorphic membrane protein (fragment).
OS Chlamydia psittaci (Chlamydia phila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_taxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RT serotype-1 Chlamydia psittaci strains."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243418; AAL36962.1; -.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_pmp.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01414; autotrans_barl; 1.
FT NON_TER 1
SQ SEQUENCE 602 AA; 65562 MW; CA486CFACEC131E2 CRC64;

Alignment Scores:
Pred. No.: 1,08e-64 Length: 602
Score: 1237.00 Matches: 261
Percent Similarity: 59.25% Conservative: 104
Best Local Similarity: 42.37% Mismatches: 205
Query Match: 22.87% Indels: 46
DB: 2 Gaps: 14

US-09-428-122-1 (1-3000) x Q8VU49 (1-602)
QY 1130 GGTGATCTGCTTTTGTAGGGAATACAGTCTACTTCTACTCTCGGACGAAT----- 1183
Db 2 GlyAspIleThrPheAspGlyAsnLysIleIleThrThrSerArgSerSerThrVal 21
QY 1184 ---AGAACTAGTATCGATCTAGGACGAGTGCAGAGATGCAAGATGACAGCTTTGCTCTCTGCT 1240
Db 22 LysArgAsnSerIleSerLeuGlySerGlyGlyLysPheThrLysLeuAsnAlaLysGlu 41
QY 1241 GGTAGAGCCATCTCTCTCTATGATCCCATATA---ACTACAGGATCATCCACACAGTTACA 1297
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Db 42 GlyPheGlyIlePhePheTyrAspProIleAlaAsnThrGlyAspThrAsnThrGluIle 61
 QY 1298 GATGCTTTAAAGTTAATGAGACTCCGCGAGATTCTGCACATACATAACAGGGAACATC 1357
 Db 62 GluLeuAsnLysAlaGlu-----GlyGlySerThrThrTyrThrGlyLysIle 77
 QY 1358 ATCTTCACAGAGAAAGTTATCAGACAGAGCGCGAGATTCTPAAAAATCTTACTTCG 1417
 Db 78 ValPheSerGlyGluLysLeuSerAspGluGluLysLysValAlaAspAsnLeuLysSer 97
 QY 1418 AAGTACTACAGCTGTAACTCTTCAGGAGTACTCTATCTTTAAACATGGAGTACT 1477
 Db 98 TyrPheThrGlnProLeuLysIleGlyAlaGlySerLeuValLeuLysAspGlyValThr 117
 QY 1478 CTGCAGACTCAGGCATCTCACTCAACAGCGAGATTCTCGTCTCGAATGGACGATAGAACT 1537
 Db 118 LeuGluAlaLysLysValSerGlnThrAspGlySerThrValValMetAspLeuGlyThr 137
 QY 1538 ACTTAGAACCTGCT-----GATACAGACACATAAACAATTTGGTCATTAACATC 1588
 Db 138 ThrLeuGlnThrSerSerGlyGluThrIleThrLeuThrAsnLeuAspIleAsnVal 157
 QY 1589 ACTTCTATAGCGGTGCA-----AAGAAGCGAAATAGAACCAAGCTAGC 1636
 Db 158 AlaSerLeuGlyGlyGlyGlyValAlaProAspProAlaLysValGluAlaGlnAlaSer 177
 QY 1637 TCMAAAATCTGACTTTATCTGGAACCATCTTATTCGACCGCGACGCGCAGCTTTAT 1696
 Db 178 GlyLysThrValThrIleAsn--AlaValAsnLeuValAspThrAspGlyAsnAlaTyr 196
 QY 1697 GAAATCATPAGTTAAGAAATCCTCAGCTCCTAGCATCTTAGAGCTCAAGCTCTGGA 1756
 Db 197 GluTyrProIleLeuAlaThrSerGlnProPheThrAlaIleAlaLysAlaGlySer 216
 QY 1757 ACTGTAACAGACCCGCTGACTCCAGAT-----CCTATAATGGGT 1798
 Db 217 SerGlyThrThrThrThrProThrAspAsnLeuLysAsnTyrThrProThr----- 234
 QY 1799 GAGAAATTCATCCATCAGCGCTATCAGGGAACCTTGGGCGCCCAATTGTTTGGGGACAGGGCT 1858
 Db 235 -----HisTyrGlyTyrGlnGlyAsnTrp--ThrValThrTrpLysLeuGlyThr 250
 QY 1859 TCTACG-----ACTGCAACCTTCAACTGAGCTAAACCTGGCTATATTCCTAATCCC 1909
 Db 251 SerAlaGlnGluGluThrAlaThrLeuThrTrpGluGlnThrAspTyrSerProAsnPro 270
 QY 1910 GACGCTATCGGCTCTTATAGTCCCTAATAGCTTATGAAATGCAATTTATAGATATGCTCT 1969
 Db 271 GluArgGlnGlyProLeuValProAsnThrLeuTrpGlySerPheSerAspIleArgAla 290
 QY 1970 CTCATTATCTTATGAGACTCGAAACGAAAGGCTTCGAGGAGACCGCTGCTTTTGGTGT 2029
 Db 291 IleGlnAsnLeuIleAspIleSerValAsnGlyAlaAspTyrArgGlyPheTrpVal 310
 QY 2030 GTGGATTATCTAATCTTTCCATAGGATAGTACAAAACACAGACGCGGGTTCCCAT 2089
 Db 311 SerGlyLeuGlyAsnPheLeuHisLysSerGlySerAsnThrLysArgLysPheArgHis 330
 QY 2090 TTGAGTGGCGGTATGTCATAGAGGAAACCTACATCTGTTTCAGATAAGATCTTAGT 2149
 Db 331 HisSerAlaGlyTyrAlaLeuGlyValTyrAlaGlnThrSerThrGluAspValPheSer 350
 QY 2150 GCTGCATTTGTAGCTCTTTGGAAGAGATAGACTTACTTTGTAGCTAAGAATCAAGGT 2209
 Db 351 AlaAlaPheCysGlnLeuPheGlyLysAspLysAspTyrPheValSerLysAsnSerSer 370
 QY 2210 ACAGTCTACGAGGAACCTCTTATACAGACAAACCACTATATCTCTCTCTCTTCG 2269
 Db 371 AsnIleTyrAlaGlySerIleTyrGlnHisIleSerTyrTrpAsnAlaTrpGlnAsn 390
 QY 2270 AAATACGGCCTTGTGCTTATAGTCTTCTACAGAGATTCCTGCTCTCTTTTCAGGA 2329
 Db 391 LeuLeuGln-----SerThrIleGlyAlaGluAlaProLeuValLeuAsnAla 406

QY 2330 AACCTTAGTACACCCATACGATACGATCTGAAACCAAGTATACA----- 2377
 Db 407 GlnLeuThrTyrCysHisAlaSerAsnAsnMetLysThrAsnMetThrAsnThrTyrVal 426
 QY 2378 -----ACATATCTCTACTGTTTAAAGAAAGCTGGGGGAATGATAGTTTCGCTTTA 2425
 Db 427 ProLysAsnValThrLeuSerGluIleLysGlyAspTrpGlyAsnAspCysPheGlyVal 446
 QY 2426 GAATTCGGTGGAGAGCTCCGATTTCGTAGTAAAGAGTGTCTTATTGACAGTACATG 2485
 Db 447 GluPheGlyAlaMetAlaProIleGluThrProSerSerPheLeuPheAspArgTyrSer 466
 QY 2486 CCTTCATGAATTCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGACACGGGAACA 2545
 Db 467 ProPheLeuGlnLeuGlnLeuValHisAlaHisGlnAspAspPheLysGluAsnAsnSer 486
 QY 2546 --GAAGCTCGTGAATTGGGAAGTAGCGCTCTGTGAATCTTGCTTACCTATCGGGATC 2602
 Db 487 AspGlnGlyArgTyrPheGluSerSerAsnLeuThrAsnLeuSerMetProIleGlyIle 506
 QY 2603 CGATTGTATAAGGAATCAGACTGCCAAGATCAACGACGACAACTCAACTCTTGGTTACT 2662
 Db 507 LysPheGluArgPheAlaTyrAsnAspValAlaSerTyrHisLeuThrAlaAlaTyrAla 526
 QY 2663 GTGGATCTTGTCTAGTAAACCCGACTGTAGCACAACACTGCGAATTAGCGGTGATTCT 2722
 Db 527 ProAspIleValArgSerAsnProAspCysThrAlaSerLeuLeuValSerProThrSer 546
 QY 2723 -----TCGAAAACCTTCGCTACGAAATTTGGCAGACAAAGCTTTAGTCTCTCGTCAGGG 2776
 Db 547 AlaValTrpValThrLysAlaAsnAsnLeuAlaArgSerAlaPheMetLeuGlnAlaGly 566
 QY 2777 AACCAATTTTGTCTTAACTCAAAATTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGT 2836
 Db 567 AsnTyrLeuAlaLeuSerHisAsnMetGluLeuPheSerGlnPheGlyPheGluIleArg 586
 QY 2837 GGGTATCTCCCAATTAACATGTAGCTAGGACGAGCAAAATACCAATTC 2884
 Db 587 GlySerSerArgThrTyrAsnValAspLeuGlySerLysIleGlnPhe 602
 RESULT 7
 Q8VL57 PRELIMINARY; PRT; 601 AA.
 ID Q8VL57; AC
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative polymorphic membrane protein (Fragment).
 OS Chlamydia psittaci (Chlamydia phila psittaci).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
 OX NCBI_TaxID=83554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=POS, and LUG;
 RA Laroucau K., Souriau A., Rodolakis A.;
 RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
 RL serotype-1 Chlamydia psittaci strains."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF243416; AAL36960.1; --
 DR EMBL; AF243417; AAL36961.1; --
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 601 AA; 65476 MW; D6AA97EC9072C757 CRC64;
 Alignment Scores:
 Pred. No.: 1,15e-63 Length: 601
 Score: 1219.50 Matches: 259
 Percent Similarity: 59.25% Conservative: 106
 Best Local Similarity: 42.05% Mismatches: 204

Query Match:	22.55%	Indels:	47
DB:	2	Gaps:	15
US-09-428-122-1 (1-3000) x Q8VL57 (1-601)			
QY	1130	GGTACATTGCTTTTATAGGAATACAGTCACTTCTACTACTCTCTGGGACGAAT-----	1183
DB	2	GlyAspIleThrPheAspGlyAsnLysIleIleThrThrSerArgSerSerSerThrVal	21
QY	1184	---AGAAGTAGTATCGACTTAGGAACGAGTGCAGAGATGACAGCTTTGCGTTCGCTGCT	1240
DB	22	LysArgAsnSerIleSerLeuGlySerGlyGlyLysPheThrLysLeuAsnAlaLysGlu	41
QY	1241	GGTAGAGCCATCTACTTCTATGATCCCATATA---ACTACAGGATCATCCCAACAGTTACA	1297
DB	42	GlyPheGlyIlePhePheThrAspProIleAlaAsnThrGlyAspThrAsnThrGluIle	61
QY	1298	GATGCTTTAAAGTTAATGAGACTCCGCGAGATTCTGCACATACATAATACAGGGAACATC	1357
DB	62	GluLeuAsnLysAlaGlu-----GlyGlySerThrThrThrThrGlyLysIle	77
QY	1358	ATCTTCACAGAGAAAAGTTATCAGAGACAGAGCGCGAGATCTCTAAATCTTACTTCG	1417
DB	78	ValPheSerGlyGluLysLeuSerAspGluGluLysLysValAlaAspAsnLeuLysSer	97
QY	1418	AAGCTACTACAGCTGTAACTCTTTACAGAGTACTCTATCTTTAAACATGAGTGAAT	1477
DB	98	TyrPheThrGlnProLeuLysIleGlyAlaGlySerLeuValLeuLysAspGlyValThr	117
QY	1478	CTGCAGACTCAGGCATTCCTCAACAGGAGATTCCTCTCGAATGAGCTAGTAACT	1537
DB	118	LeuGluAlaLysLysValSerGlnThrAspGlySerThrValValMecAspLeuGlyThr	137
QY	1538	ACTCTAGAACCTGCT-----GATACCTAGCACCATATAAACAATTTGGTTCATTAACATC	1588
DB	138	ThrLeuGlnThrSerSerSerGlyGluThrIleThrLeuThrAsnLeuAspIleAsnVal	157
QY	1589	AGTTCTATAGACGGTGCA-----AAGAAGCGAATAATAGAACCAAGCTACG	1636
DB	158	AlaSerLeuGlyGlyGlyValAlaProAspProAlaLysValGluAlaGlnAlaSer	177
QY	1637	TCAAAAATCGACTTATTCGGAACCATCACTTTATTGGACCCGCGGCGGCGTTTAT	1696
DB	178	GlyLysThrValThrIleAsn---AlaValAsnLeuValAspThrAspGlyAsnAlaThr	196
QY	1697	GAATATCATAGTTAAGAAATCCTCAGTCTCAGCATCTTAGAGCTCAAGACTCTGGA	1756
DB	197	GluThrProIleLeuAlaThrSerLysProPheThrAlaIleAlaLysAlaGlySer	216
QY	1757	ACTGTAACAGCACCGCAGTGAATCCAGAT-----CCTATAATGGGT	1798
DB	217	SerGlyThrThrThrThrProThrAspAsnLeuLysAsnThrThrProThr-----	234
QY	1799	GAGAAATTCATAGCTATCAGGACTCAGGAACTCGGGCCCAATTTGTTGGGGACAGGGCT	1858
DB	235	-----HisThrGlyThrGlnGlyAsnThrPheThrValThrThrLysLeuGlyThr	250
QY	1859	TCTACG-----ACTGCAACCTTCAACTGAGCTTAAACCTGGCTATATCTCTAATCCC	1909
DB	251	SerAlaGlnGluThrAlaThrLeuThrThrThrGluThrAspThrProAsnPro	270
QY	1910	GAGCGTATCGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATTAATGCTCT	1969
DB	271	GluArgGlnGlyProLeuValProLysThrLeuThrGlySerPheSerAspIleArgAla	290
QY	1970	CTCCATTATCTATGAGACTGCAACAGAGGTTCCAGGAGACCGCTCTTTGCTGT	2029
DB	291	IleGlnAsnLeuIleAspIleSerValAsnGlyAlaAspThrArgArgGlyPheThrVal	310
QY	2030	GCTGGATTATCTAATCTTCTCCATAGGATAGTACAAAACACAGCGCGGGTTCCGCCAT	2089
DB	311	SerGlyLeuGlyAsnPheLeuHisLysSerGlySerAsnThrLysArgLysPheArgHis	330
QY	2090	TTGAGTGGCGGTTATGTCATAGCAGGAAACCTACATACTTGTTCAGATAAGATCTTTAGT	2149
DB	331	HisSerAlaGlyThrAlaLeuGlyValThrAlaGlnThrSerThrGluAspValPheSer	350
QY	2150	GCTGCATTTTGTGCTCTTTTGAAGAGATAGAGACTACTTTGTAGTAGAATCAAGGT	2209
DB	351	AlaAlaPheCysGlnLeuPheGlyLysAspLysAspThrPheValSerLysAsnSerSer	370
QY	2210	ACAGTCTACGGAGAACTCTATTACAGCACACAAACCACTATATCTCTCTCTCTTC	2269
DB	371	AsnIleThrAlaGlySerIleThrGlnHisIleSerThrThrAsnAlaThrGlnAsn	390
QY	2270	AAACTACGGCGCTTCTGTTGCTTATGTTCTTACACAGATTTCTGTTCTCTTTTCAGGA	2329
DB	391	LeuLeuGln-----SerThrIleGlyAlaGluAlaProLeuValLeuAsnAla	406
QY	2330	AACCTTAGCTACACCCCATACGGATACAGTCTGAAACCAAGTATACA-----	2377
DB	407	GlnLeuThrThrCysHisAlaSerAsnAsnMetLysThrAsnMetThrAsnThrThrVal	426
QY	2378	-----ACATATCTCTGTTTAAAGGAGCTGGGGGATGATAGTTTCGCTTTA	2425
DB	427	ProLysAsnValThrLeuSerGluIleLysGlyAspThrGlyAsnAspCysPheGlyVal	446
QY	2426	GAATTCGGTGAAGAGCTCCGATTTGCTTAGATGAAAGTGTCTATTGTAGCAGTACATG	2485
DB	447	GluPheGlyAlaMetAlaProIle---GluAsnAlaSerPheLeuPheAspArgThrSer	465
QY	2486	CCCTTCATGAAATTCGAGTTTGTCTATGCACATCAGGAAGGTTTTTAAAGACAGGGAACA	2545
DB	466	PropheLeuGlnLeuGlnLeuValHisAlaHisGlnAspPheLysGluAsnAsnSer	485
QY	2546	---GAAGCTCGTGAATTTGGAGTAGCGCTTGTGATCTTGTCTTACCTTACCTATCGGATC	2602
DB	486	AspGlnGlyArgThrPheGluSerSerAsnLeuThrAsnLeuSerMetProIleGlyIle	505
QY	2603	CGATTGTATAGGAATCAGACTGCCAAGATGCAACATCAATCTAACCTCTTGTGTATACT	2662
DB	506	LysPheGluArgPheAlaThrAsnAspValAlaSerThrHisLeuThrAlaAlaThrAla	525
QY	2663	GTGGATCTTGTTCGTAGTAAACCCGACGTGTACGACACACTCGCAATTTAGCGGTATCT	2722
DB	526	ProAspIleValArgSerAsnProAspCysThrAlaSerLeuLeuValSerProThrSer	545
QY	2723	-----TGAAAACTTCGGTACGAAATTTGCAAGACAGCTTTAGTCTCTCGTCAAGG	2776
DB	546	AlaValThrValThrLysAlaAsnLeuAlaArgSerAlaPheMetLeuGlnAlaGly	565
QY	2777	AACCATTTTGTCTTAACTCAAAATTTGAAGCTTTAGCAATTTCTTTGAAATGCGT	2836
DB	566	AsnThrLeuAlaLeuSerHisAsnMetGluLeuPheSerGlnPheGlyPheGluIleArg	585
QY	2837	GGGTCTATCTGCAATTAACAATGTAGCTTAGGACGAGCAAAATCCAAATC	2884
DB	586	GlySerSerArgThrThrAsnValAspLeuGlySerLysLysIleGlnPhe	601
RESULT 8			
ID	Q8VU50	PRELIMINARY;	PRT; 700 AA.
AC	Q8VU50;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
OS	Putative polymorphic membrane protein (Fragment).		
OC	Chlamydia psittaci (Chlamydia phila psittaci).		
OX	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaaceae; Chlamydia phila.		
NCBI	NCBI_TaxID=83554;		
SEQUENCE	SEQUENCE FROM N.A.		
RC	STRAIN=POS;		
RA	Laroucau K., Souriau A., Rodolakis A.;		
RT	"Isolation of a new pmp sequence and evidence of pmp polymorphism in		
RT	serotype-1 Chlamydia psittaci strains."		

Wed Dec 17 09:17:08 2003

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF243415; AAL36959.1; -
 DR InterPro: IPR003368; Chlamydia_PMP.
 DR Pfam: PF02415; DUF145; 1
 DR TIGRFAMs: TIGR01376; POMP_repeat; 3.
 FT NON_TER 700 700
 SQ SEQUENCE 700 AA; 74200 MW; 2C38E504F48D1D1 CRC64;

Alignment Scores: 4.48e-61 Length: 700
 Pred. No.: 1175.50 Matches: 291
 Score: 1175.50
 Percent Similarity: 50.00% Conservative: 123
 Best Local Similarity: 35.14% Mismatches: 237
 Query Match: 21.73% Indels: 177
 DB: 2 Gaps: 2

US-09-428-122-1 (1-3000) x Q8VU50 (1-700)

QY 89 ATATATTTCACATGAAGTCTCTTCCCAAGTTTGTATTCTACATTTGCTATTTC 148
 Db 5 ValTyrTrpPheLeuLeuSerSer-----SerLeuLeuAlaSerAsn 18
 QY 149 CCTTGTCTATGATT---GCTACCGACAGTTTTGGATTCAAGTGGAGTTTCGATGGG 205
 Db 19 SerLeuSerPheAlaGlnValThrAsnGluThrLeuThrSerSerAspSerTyrAsnGly 38
 QY 206 AAT---AAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACCTAC 262
 Db 39 AsnValThrSerAspGluPheGluValLysGluThr-----ThrSerGlyAlaLeuTyr 56
 QY 263 CTATTTAAGGAATATGCTACTCTAGAAAATATCTCTGGAACAGCAGCAATCACAAAA 322
 Db 57 ThrCysGluGlyAsnValCysIle---SerTyrAlaGlyLysAspSerProLeuAsnLys 75
 QY 323 AGCTGTTTAAACACATAAGGGGATTTGACTTTTCACAGTAAACGGAACTCTCTATTG 382
 Db 76 SerCysPheSerGluThrThrGluAsnLeuSerPheIleGlyAsnGlyTyrThrLeuCys 95
 QY 383 TTCCAAACGGTGGATGTCAGGAGCTGTAGCAGGGCTGCTGTTAATACAGAGGCTGGTAGAT 442
 Db 96 PheAspAsnIleThrThrAlaSerAsnProGlyAlaIleAsnValSerGlyAspGln 115
 QY 443 AAATCTACACGTTTATAGGTTTCTCGCTATCTTTATTCGCTCTCCGGAAGTCG 502
 Db 116 LysThrLeuAsnValSerGlyPheSerLeuPheSerCysAlaHisCysProGly--- 134
 QY 503 ATAATCTCCGCAAGGAGCGGTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAAAT 562
 Db 135 ---ThrThrGlyTyrGlyAlaIleGln-----ThrLysGly 145
 QY 563 GTCAGTTTGTCTTTCAGCAAAAACCTTTTCAACGGGATAATGCGGTGCTATCCGCCAAAA 622
 Db 146 ValSer----- 147
 QY 623 ACTCTTTCATTAACAGGACTACATGTCTGCTGTTTCTGAAAATACCTCTCCTCAAG 682
 Db 147 ----- 147
 QY 683 AAAGCGGAGCATTCAGACTTCCGATGCCCTTACCATTACTGTGAAACCAAGGGGAAGTC 742
 Db 147 ----- 147
 QY 743 TCTTTTCTGCAATATCTTCTCGGATTCGGAGCTGCAATTTTACAGAGCCTCGGTG 802
 Db 147 ----- 147
 QY 803 ACTATTCTAATAGCTAAAGTTTCCTTTATNTGACAAATAGGTACAGGAGCGAGCTCC 862
 Db 148 ThrPheSerGlyAsnAsnLysLeuIlePheAspAsnAsnCysSerThrGly----- 164
 QY 863 TCACAAACGGGATATGTCAGAGGTGCTATC---TGTGCTTATAAACTAGTACAGAT 919
 Db 165 -----GluGlyGlyAlaIleLysCysAla-----ThrGlySerAsn 176

QY 920 ACTAAGTCAACCTCAGTGAATCAGATGTTACTCTTACAGCAACAATACATACGCAACA 979
 Db 177 AlaGluLeuLysLeuGluGlyAsnSerTyrValValPheSerGlyAsnSerSerGlnLys 196
 QY 980 GCGGAGGAGCTATCTATGTGAAAAAGCTCGAAGTGGCTTCGGAGGACTTACCCCTATTC 1039
 Db 197 LysGlyGlyAlaIleTyrThrLysLysLeuThrIleThrAlaAspGlyProThrLeuPhe 216
 QY 1040 AGTAGAATAGTGTCAATGGAGGTACAGCTCTTAAGGTGGAGCCATAGCTACGAAGAT 1099
 Db 217 SerAsnAsnSerValSer---AlaSerSerProLysGlyGlyAlaIleCysLeuAspAsp 235
 QY 1100 ---AGTGGGAGTTCAGTTTATCCCGCATAGTGGTGACATTGCTTTTACGGGAATACA 1156
 Db 236 ThrSerSerGluCysSerLeuThrAlaAsnLeuGlyAspIleThrPheAspGlyAsnLys 255
 QY 1157 GTCACCTTCTACTCTCTGGGACGAAT-----AGAAGTAGTATCGACTTAGAAGC 1207
 Db 256 ValIleLysThrAsnGlyGlySerThrValLysArgAsnAlaIleAspLeuGlySer 275
 QY 1208 AGTGCAAGATGACAGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267
 Db 276 GlyGlyLysPheThrLysLeuAsnAlaLysGluGlyPheGlyIlePhePheHisAspPro 295
 QY 1268 ATA---ACTACAGGATCATCCACACAGTTACAGATGCTCTTAAAGTTAATGAGACTCCG 1324
 Db 296 IleAlaAsnThrGlyGlySerThrGluIle-----GluLeuAsnLysThrGlu 311
 QY 1325 GCAGATTCTGCATCAATATACAGGGAACATCATCTTACAGGAGAAAAGTTATCAGAG 1384
 Db 312 SerAspThr-----TyrThrGlyLysIleValPheSerGlyGlyLysLeuSerAsp 329
 QY 1385 ACAGAGCCGCAATCTTAAATCTTACTTCAAGCTACTACAGCTGTAACCTCTTTCA 1444
 Db 330 GluGlyLysThrValProAspAsnLeuLysSerTyrPheLysGlnProLeuLysIleGly 349
 QY 1445 GGAAGTACTCTATCTTTTAAACATGGAGTACTCTGCAGACTCAGCACTCACTCAACAG 1504
 Db 350 AlaGlySerLeuValLeuLysAspGlyValThrLeuGluAlaLysLysIleThrGluThr 369
 QY 1505 GCAGATTCTCTCGTCTCGAATGAGCTAGGAATCTCTAGAA-----CCTGCT 1552
 Db 370 LysGlySerThrValValMetAspLeuGlyThrThrLeuGlnThrProSerSerSerGly 389
 QY 1553 GATCTAGCACCATAACAATTTGCTCATTAACATCAGTTCTATA-----GACGGT 1603
 Db 390 GluThrIleThrLeuThrAsnLeuAspIleAsnIleAlaSerLeuGlyGlyGlyGly 409
 QY 1604 GCAAGAAGGCAAAATAGAAACCAAGCTACGTCACAAAATCTGACTTTTATCTGGAACC 1663
 Db 410 ThrAlaProAlaLysLeuAlaThrAsnThrAlaSerGlnAlaIleSerIleAla---Ala 428
 QY 1664 ATCACTTTATGGACCGGACCGGACCGTCTTATGAAAATCATAGTTTAAAGAAATCCTCAG 1723
 Db 429 ValAsnLeuValAsnThrAspSerAsnThrTyrGluAspProIleLeuSerAlaSerLys 448
 QY 1724 TCCTACGACATCTTAGAGCTCAAGCTTCTGGAAGTCTTAACAACGCGAGTCACTCCA 1783
 Db 449 SerPheSerAlaIle-----ThrAlaThrThrSerSerSerThrValThrPro 464
 QY 1784 GATCCTATATGGGTGAGAAATTC-----CATTCAGGCTATCAGGGAACTTGG 1831
 Db 465 ProGluThrAsnLeuLysAsnTyrThrProThrHisTyrGlyTyrGlnGlyAsnTrp 484
 QY 1832 GGCCTAATTTGGGGACAGGGGCTTCT-----ACGACTGCAACCTCACTCAGTGG 1882
 Db 485 ---ThrLeuAlaTrpProProGlyGluThrMetGlnLeuLysThrAlaThrLeuAsnTrp 503
 QY 1883 ACTAAACCTGGCTATATCTTAATCCGAGGTATCGGCTCTTAGTCCCTTAATAGCTTA 1942
 Db 504 GluGlnThrGlyTyrSerProAsnProGluArgValGlySerLeuValProAsnThrLeu 523

QY 2150 GCTGCAATTTGTCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGCAATCAAGGT 2209
Db 351 AlaAlaPheCysGlnLeuPheGlyLysAspLysAspTyrPheLeuSerLysAsnSerSer 370
QY 2210 ACAGTCTACGGAGGAACTCTCTATTACCAAGCAACAGAAACCTATATCTCTCTCTTCG 2269
Db 371 ThrIleTyrAlaGlySerIleTyrGlnHis 381
QY 2270 AAACCTACGGCCTTTGTTGCTGCTTAT 2296
Db 382 1leSerTyrTrpAsnAlaTrpGlnAsnLeuLeuGlnAsnThr 395
QY 2297 GTTCCTACAGATTCCTGTTCTCTTTCCAGAACTTAGCTACACCCATACGATAC 2356
Db 396 IleGlyAlaGluAlaProLeuValLeuAsnAlaGlnLeuThrTyrCysHisAlaSerAsn 415
QY 2357 GATCTCAAAACCAAGTATACA 2392
Db 416 AsnMetLysThrAsnMetThrAsnThrTyrThrProLysAsnValThrProSerGluIle 435
QY 2393 AAAGGAAGCTGGGGGAATGATGTTTCGCTTTAGAAATCGGTGGAGAGCTCGATTCG 2452
Db 436 LysGlyAspTrpGlySerAspCysPheGlyValGluPheGlyAlaLysAlaProIle 454
QY 2453 TTAGATCAAGTCTCTATTGACGAGTACATGCCCTTCATGAAATTCGAGTTTGTCTAT 2512
Db 455 GluThrAlaSerLeuLeuPheAspMetTyrSerProPheValLysLeuGlnLeuValHis 474
QY 2513 GCACATCAGGAGGTTTAAAGAACAGGGAACA 2569
Db 475 AlaHisGlnAspPheLysGluAsnSerAspGlnGlyArgTyrPheGluSerAsn 494
QY 2570 CGTCTTGTAATCTGCTTACTATCGGATCCGATTCGATGAGGAAATCAGACTGCCAA 2629
Db 495 AsnLeuThrAsnLeuSerMetProIleGlyValLysLeuGluLysPheSerHisGluAsp 514
QY 2630 GATGCAAGTACATCTACTCTGTTGTTACTGTGATCTGTTGTTAGTACCCCGAC 2689
Db 515 ThrAlaSerTyrAsnLeuThrLeuAlaTyrAlaProAspIleValArgSerAsnProAsp 534
QY 2690 TGTACGACAACTCGCAATTAGCGGTGATTCT 2743
Db 535 CysThrAlaSerLeuLeuValSerProThrSerAlaValTrpValThrLysAlaAsnAsn 554
QY 2744 TTGGGAAGCAAGCTTTAGCTTCGTCGAGGAAACATTTTGTCTTAACTCAAAATTT 2803
Db 555 LeuAlaArgHisAlaPheIleLeuGlnAlaGlyAsnTyrLeuAla 569
QY 2804 GAAGCCTTTAGCAATTTCTTTTGAATTGCGTGGGTCACTCGCAATTACAATGTAGAC 2863
Db 570 570 -----ThrTyrAsnIleAsp 574

RESULT 10

Q9RB67 ID Q9RB67 PRELIMINARY; PRT; 445 AA.
AC AC
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pmp 5.
GN Pmp 5.2.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiales.
ON NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL Nucleic Acids Res. 28:2311-2314 (2000).
DR EMBL; AP002545; BAA98231.1; -
DR InterPro; IPR006315; Autotransport.
DR Pfam; PF03797; Autotransporter.
DR TIGRfams; TIGR01414; autotrans_bar1; 1.
SQ SEQUENCE 445 AA; 49353 MW; EFA24AFC9C5097A6 CRC64;

Alignment Scores:

Pred. No.: 7,966-52 Length: 445
Score: 1017.50 Matches: 202
Percent Similarity: 60.99% Conservative: 70
Best Local Similarity: 45.29% Mismatches: 165
Query Match: 18.81% Indels: 9
DB: 16 Gaps: 7

US-09-428-122-1 (1-3000) x Q9RB67 (1-445)

QY 1565 ATAAACAATTGGTTCATTAAACATCATGTTCTATAGACGGTGCAGAGCAAGCAAAATAGAA 1624
Db 3 1leThrAsnLeuSerIleAsnAlaAspThrIleTyrGlyAsnProIleAsnIleVal 22
QY 1625 ACCAAGCTACGTCATAAAATCTGACTTTATCTCGAACCATCACCTTTATTGGACCGACG 1684
Db 23 AlaSerAlaAlaAsnLysAsnIleThrLeuThrGlyThrLeuAlaLeuValAsnAlaAsp 42
QY 1685 GGCAGCTTTTATGAAATCATAGTTTAAAGAAATCTCTAGTCCTACGACATCTTAGAGTCT 1744
Db 43 GlyAlaPheTyrGluAsnHisThrLeuGlnAspSerGlnAspTyrSerPheValLysLeu 62
QY 1745 AAA-----GCTTCTGGAACCTGTAACAGCACCGCAGTACTCCAGATCCT-----ATA 1792
Db 63 SerProGlyAlaGlyGlyThrIleThrGlnAspAlaSerGlnLysProLeuGluVal 82
QY 1793 ATGGGTGAGAAATTCCTACCGCTATCAGGAACTTGGGGC---CCAATTGTTGGGG 1849
Db 83 AlaProSerArgProHisTyrGlyTyrGlnGlyHisTrpAsnValGlnValIleProGly 102
QY 1850 ACAGGGGCTTCT---ACGACTGCACCTTCAACTGACTTAAACTGGCTATATCTCTAAT 1906
Db 103 ThrGlyThrGlnProSerGlnAlaAsnLeuGluTrpValArgThrGlyTyrLeuProAsn 122
QY 1907 CCGAGCGTATCGCTCTTTAGTCCCTATAGCTTATAGTGAATGCATTTATAGATATAGC 1966
Db 123 ProGluArgGlnGlySerLeuValProAsnSerLeuTrpGlySerPheValAspGlnArg 142
QY 1967 TCTCTCCATTATCTTATGAGACTGCAGAAAGGTTGCAGGGAGACCGTCTTTTGG 2026
Db 143 AlaIleGlnGluIleMetValAsnSerSerGlnIleLeuCysGlnGluArgGlyValTrp 162
QY 2027 TGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAACACGACCGGGTTTCG 2086
Db 163 GlyAlaGlyIleAlaAsnPheLeuHisArgAspLysIle---AsnGluHisGlyTyrArg 181
QY 2087 CATTGAGTGGCGGTTATGTCATAGGAGGAACCTACATCTTGTTCAGATAAGATCTT 2146
Db 182 HisSerGlyValGlyTyrLeuValGlyValGlyThrHisAlaPheSerAspAlaThrIle 201
QY 2147 AGTCTGCATTTTGTTCAGCTCTTTGGAAGAGACTAGACTACTTTGTAGCTAAGATCAA 2206
Db 202 AsnAlaAlaPheCysGlnLeuPheSerArgAspLysAspTyrValValSerLysAsnHis 221
QY 2207 GGTACAGTCTACGAGGAACTCTCTATTACCACCAACGAAACCTATATCTCTCTCT 2266
Db 222 GlyThrSerTyrSerGlyValValPheLeuGluAspThrLeuGluPheArgSer---Pro 240
QY 2267 TGAACACTACGGCTTGTGTTGTTCTTATGTTCTTCTACAGAGATTCCTGTTCTTCTTCA 2326
Db 241 GlnGlyPheTyrThrAspSerSerSerGlnAlaCysCysAsnGlnValValThrIleAsp 260


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Db 309 ValSerPheGluMetLysTrpValSerThrGlyTyrIleProThrAlaAsnArgAla 328
QY 1922 TCCTTAGTCCCTAAGCTTATGGAATGCAATTTATAGATATTGCTCTCTCCATTTCTT 1981
Db 329 ThrLeuValProAsnSerValTrpCysSerAlaIleAspMetArgAlaPheGlnAsnLeu 348
QY 1982 ATGGAGACTGCAAAAGAGGGTTGAGGAGACCGTCTTTTGTGTGTGCTGGATATCT 2041
Db 349 ValGluValSerThrGluGlyAspPheHisArgGlyLeuTrpIleSerGlyIleSer 368
QY 2042 RACTTCTTCCATAAGATAGTACAAAACACAGCAGCGGTTTCGCCATTTAGTGGCGGT 2101
Db 369 AsnPhePheHisLysAspSerThrLysValGlnGluGlyPheArgHisIleSerSerGly 388
QY 2102 TATGTCATAGAGGAACCTACATCTTCTTCAGATAAGATTCTTAGTGTCTCCATTTGT 2161
Db 389 TyrValValGlyValSerThrGlnProIleSerAsnLysValMetAspLeuAlaPheCys 408
QY 2162 CAGCTCTTTGGAAGATAGAGACTACTTTGTAGCTAAGATCAAGGTACAGTCTACGGA 2221
Db 409 GlnMetLeuGlySerLysAspTyrArgLeuAlaAspAlaArgSerHisValTyrAla 428
QY 2222 GGAACCTCTATTACAG-----CACACGAAACCTATATCTCTCTCTCT 2266
Db 429 AlaSerIleHisThrLysCysGluLysLeuValAsnHisTyrThrPhe----- 444
QY 2267 TGCAAACTACGGCCTTGTGTTGCTTATGTTCTCTACAGATATCTCTTCTTTTCA 2326
Db 445 SerLysArgLysGlyAlaIleLeuAlaArgLysProGluLysSerProIleIlePheAsp 464
QY 2327 GGAACCTTAGCTACACCATACGGATACAGTCTGAAACCAAGTATACACATATCT 2386
Db 465 AlaGlnLeuSerTyrSerLeuSerHisAsnSerMetThrThrLysHisThrProAsnPro 484
QY 2387 ACTGTTTAAAGAGCTGGGGGATGATAGTTTCGCTTTAGAAATTCGGTGGAAAGCTCG 2446
Db 485 SerSerArgGlyLysTrpAsnAsnHisCysValAlaGlyGluLeuGlySerTyrLeuPro 504
QY 2447 ATTTGCTTAGATGAAAGTCTCTATTGAGCAGTACATGCCCTTCAGAAATTCGAGTTT 2506
Db 505 IleLeuValAspHisProAlaIle---GluGluLeuPheProPheValLysLeuHisIle 523
QY 2507 GTCTATGTCATCAGAGAGGTTTAAAGAACAG-----GGAACAGAGCTCGTGAATTT 2560
Db 524 ValPheValGlnGlnGluAspPheLysGluThrGlnGlyGlyThrGluAsnArgAsnPhe 543
QY 2561 GGAAGTAGCCGCTTGTGTAATCTTGCCTTACCTATCGGATCCGATTTGATAGGAATCA 2620
Db 544 GlnSerAlaHisPheValAsnValSerLeuProLeuGlyValArgPheGluLysThrAsn 563
QY 2621 GACTGCCAAGATGCAACGTACATCTAACTCTTGGTGTATCTGTTGATCTGTTCTAGT 2680
Db 564 LysLeuAsn-----ThrTyrAsnIleArgLeuAlaTyrGlnProAspIleTyrArgAsp 581
QY 2681 AACCCGACTGTACGACACACTCGCAATTAGCGGTGATCTTGGAAACCTTCGGTAGC 2740
Db 582 AlaProLysSerLysValPheLeuProSerValHisThrAlaIlePheSerThrGlyAlaThr 601
QY 2741 AATTTGGCAGACAAAGCTTTAGTCCTTCGTCAGGGAACCATTTTTCCTTAACTCAAAT 2800
Db 602 AsnLeuSerArgGlnAlaMetIleLeuAspGlySerAspHisHisIleThrAspAsn 621
QY 2801 TTTGAAGCCTTTAGCCAAATTTCTTTGAATTCGGTGGTCACTCCGCAATTTCAATGTA 2860
Db 622 LeuGluValPheCysHisGlyAlaPheGluLeuArgGlySerSerArgAsnTyrAsnVal 641
QY 2861 GACTTAGCAGCAAAATACCAATTC 2884
Db 642 AspIleGlyArgTyrLysPhe 649
PRELIMINARY; PRT; 186 AA.
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RESULT 12

Q9RB72

ID Q9RB72

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AC Q9RB72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Polymorphic outer membrane protein G family.
GN PMP_3_1.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RT Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL Nucleic Acids Res. 28:2311-2314 (2000).
DR EMBL: AP002545; BAA98225.1; -.
DR InterPro: IPR003368; Chlamydia_PMP.
DR Pfam: PF02415; DUF145; 1.
SQ SEQUENCE 186 AA; 19540 MW; 64557A5346533FA3 CRC64;
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Alignment Scores:

Pred. No.:	5,68e-46	Length:	186
Score:	917.00	Matches:	185
Percent Similarity:	99.47%	Conservative:	1
Best Local Similarity:	98.93%	Mismatches:	0
Query Match:	16.95%	Indels:	1
DB:	16	Gaps:	0

US-09-428-122-1 (1-3000) x Q9RB72 (1-186)

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QY 74 ATTCAAAATCAAGTATATATTTTCAATGAAGTCTTCTTCCCAAGTTGTATTCT 133
Db 1 MetGlnAsnGlnSerIleTyrPheThrMetLysSerSerPheProLysPheValPheSer 20
QY 134 ACATTTGCTATTTCCTTTGCTATGATGCTACCGACAGATTTTGATTTCAAGTGG 193
Db 21 ThrPheAlaIlePheProLeuSerMetIleAlaThrGluThrValLeuAspSerAla 40
QY 194 AGTTTCGATGGGAATAAAATCGTAATTTTTCAGTTTCGTGAGTGCAGGAAGATCGTA 253
Db 41 SerPheAspGlyAsnLysAsnGlyAsnPheSerValArgGluSerGlnGluAspAlaGly 60
QY 254 ACTACTACCTATTATTAAGGAAATGCTACTCTAGAAAATATTCCTGGAAACAGCAGCA 313
Db 61 ThrThrTyrLeuPheLysGlyAsnValThrLeuGluAsnIleProGlyThrGlyThrAla 80
QY 314 ATCACAAAAAGCTGTTTAAACAACACTAAGGCGGATTTTCACATTTCACAGGTAAACGGAAC 373
Db 81 IleThrLysSerCysPheAsnAsnThrLysGlyAspLeuThrPheThrGlyAsnGlyAsn 100
QY 374 TCTCTATTGTTCCAAACCGTGGATCGAGGACTGTAGCAGGGGCTGCTGTTAACAGCAGC 433
Db 101 SerLeuLeuPheGlnThrValAspAlaGlyThrValAlaGlyAlaAlaValAsnSerSer 120
QY 434 GTGGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTTTATTCGGTCTCTCT 493
Db 121 ValValAspLysSerThrThrPheIleGlyPheSerSerLeuSerPheIleAlaSerPro 140
QY 494 GGAAGTTCGATAACTACCGCAAGAGCGGTAGTCTGTCTACGGTAGCTTGTAGTTGTG 553
Db 141 GlySerSerIleThrThrGlyLysGlyAlaValSerCysSerThrGlySerLeuSerLeu 160
QY 554 ACAAAAATGTCAGTTTGTCTCTTCAGCAAAAACTTTTCAACGGAATAATCGCGTGTATC 613
Db 161 Thr-LysMetSerValCysSerSerAlaLysThrPheGlnArgIleMetAlaValLeuSe 180
QY 614 ACCGCAAAAACCTCTTTCAT 632
Db 180 rProGlnLysLeuPheHis 186
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US-09-428-122-1 (1-3000) x Q9RB68 (1-494)
Qy 164 GCTACCGAGACAGATTTCGATTCAGTCGAGTTTCGATCGGAATAAAATGTAAT--- 220
Db 23 AlaAlaThrThrProLeuAsnProGluAspGlyPheIleGlyGluGlyAsnThrAsnThr 42
Qy 221 TTTTCAGTTCGTGAGAGTCAGAGATGCTGGAACACTACCTACCTATTTAAAGGGAATGTC 280
Db 43 PheSerProLysSerThrThrAspAlaIleGlyThrThrTyrSerLeuThrGlyGluVal 62
Qy 281 ACTCTAGAAAATATTCCTGGACACGACAGCAGCAATACAAAAGCTGTTTAAACACACT 340
Db 63 ---LeuTyrIleAspProGlyLysGlyGlySerIleThrGlyThrCysPheValGluThr 81
Qy 341 AAGCGCGATTACCTTCACAGTACCGGAACTCTCTATTGTTCCAAACGGTGGATGCA 400
Db 82 AlaGlyAspLeuThrPheLeuGlyAsnGlyAsnThrLeuLysPheLeuSerValAspAla 101
Qy 401 GGG---ACTGTAGCAGGGGCTGCTGTTAACACGCGGTGGTAGATAAAATCTACCACTTT 457
Db 102 GlyAlaAsnIleAlaValAlaHisValGlnGlySer-----LysAsnLeuSerPhe 118
Qy 458 ATAGGGTTTCTTCGCTAFTCTTTTATPGCGTCTCCTGGAACTTCGATTAACCGGAAA 517
Db 119 ThrAspPheLeuSerLeuValIleThrGluSerProLysSerAlaValThrThrGlyLys 138
Qy 518 GGAGCGGTAGTCTCTACGGGTAGCTTGAGTTTGACAAAATAGTCAGTTTGTCTTTC 577
Db 139 GlySerLeu---ValSerLeuGlyAlaValGlnLeuGlnAspIleAsnThrLeuValLeu 157
Qy 578 AGCAAAATCTTTCACAGCAATATGCGGTGCTATCACCGCAAAACTCTTTTCATTAACA 637
Db 158 ThrSerAsnAlaSerValGluAspGlyGlyValIleLysGlyAsnSerCysLeuIleGln 177
Qy 638 GGGACTACAATGTCAGCTCTGTTTCTGAAATACCTCTCAAGAAAGCGGAGCAATT 597
Db 178 GlyIleLysAsnSerAlaIlePheGlyGlnAsnThrSerSerLysLysGlyGlyAlaIle 197
Qy 698 CAGACTTCGATCCCTTACCATTTACTGGAAACCAAGGGAAGTCTCTTTCTGACAAT 757
Db 198 SerThrThrGlnGlyLeuThrIleGluAsnAsnLeuGlyThrLeuLysPheAsnGluAsn 217
Qy 758 ACTTCTTCGATCTCGAGCTGCAATTTTACAGAAAGCTCGGTGACTATTTCTAATAAT 817
Db 218 LysAlaValThrSerGlyGlyAlaLeuAspLeuGlyAlaAlaSerThrPheThrAlaAsn 237
Qy 818 GCTAAAGTTTCCTTTATGTACATAGGTACAGGAGCGAGCTCC----- 862
Db 238 HisGluLeuIlePheSerGlnAsnLysThrSerGlyAsnAlaAlaAsnGlyGlyAlaIle 257
Qy 863 TCACACACGGGGATATGTC----- 883
Db 258 AsnCysSerGlyAspLeuThrPheThrAspAsnThrSerLeuLeuLeuGlnGluAsnSer 277
Qy 884 -----GGAGTGTCTATCTGTGCTTATAAAACTAGTACAGATATAAGGTCAAC 931
Db 278 ThrMetClnAspGlyGlyAlaLeuCys-----SerThrGlyThr---IleSer 292
Qy 932 CTCACCTGGAATCAGATGTTACTCTTCAGCAACAATACATCGACAAACAGCGGAGGAGCT 991
Db 293 IleThrGlySerAspSerIleAsnValIleGlyAsnThrSerGlyGlnLysGlyGlyAla 312
Qy 992 ATCTATGTGAAAAGCTCGAACTCGGTCGCGA---GGACTTACCTATTTCAGTAGAAT 1048
Db 313 IleSerAlaAlaSerLeuLysIleLeuGlyGlnGlyGlyAlaLeuPheSerAsnAsn 332
Qy 1049 AGTGTCAATGAGGTAGAGTCTCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAA 1108
Db 333 ValValThrHisAlaThr---ProLeuGlyGlyAlaIlePheIleAsnThrGlyGlySer 351
Qy 1109 TTGAGTTTATCCGCGGATAGTGGTGCACATTCCTTTTATAGGAAATACAGTCACTTCTACT 1168
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Db 352 LeuGlnLeuPheThrGlnGlyGlyAspIleValPheGluGlyAsnGlnValThrThr 371
Qy 1169 ACTCTCGG-----ACGAATAGAAGTAGTATCGACTTAGAAGCAGAGTCGAAAGATGACA 1222
Db 372 AlaProAsnAlaThrThrLysArgAsnValIleHisLeuGluSerThrAlaLysTrpThr 391
Qy 1223 GCTTTGGTCTGCTGCTGCTAGAGCCATCTACTTCTATGATCCATAACTACAGGATCA 1282
Db 392 GlyLeuAlaAspSerGlnGlyAsnAlaIleTyrPheTyrAspProIleThrThr---Asn 410
Qy 1283 TCCCAACAGTTACAGATGCTTAAAGTTAAATCAGACTCCGGCAGATTCTCGCACTACAA 1342
Db 411 AspThrGlyAlaSerAspAsnLeuArgIleAsnGluValSerAlaAsnGlnLysLeu--- 429
Qy 1343 TATACAGGAACATCATCTTCCAGAGGAAAGATTATCAGAGACAGAGCGCGCAGATTCT 1402
Db 430 ---SerGlySerIleValPheSerGlyGluArgLeuSerThrAlaGluAlaIle---Ala 447
Qy 1403 AAAAATCTTACTCGAAGCTACTACGCTCTACTTCTTTCAGGAGGTACTCTTCTTTA 1462
Db 448 GluAsnLeuThrSerArgIleAsnGlnProValThrLeuValGluGlySerLeuValLeu 467
Qy 1463 AAACATGAGTGAAGTCTGCACTCAGACTCAGGCATCTCAACAGGAGAGATTCTCGTCTGAA 1522
Db 468 LysGlnGlyValThrLeuIleThrGlnGlyPheSerGlnGluProGluSerThrLeuLeu 487
Qy 1523 ATGAGCTGAGAACTACTCTA 1543
Db 488 LeuAspLeuGlyThrSerLeu 494
```

RESULT 15

Q9RB70 PRELIMINARY; PRT; 427 AA.

AC Q9RB70; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)

DE Polymorphic outer membrane protein G family.

FM 4.1.

OS Chlamydia pneumoniae (Chlamydophila pneumoniae).

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.

OX NCBI_TaxID=83558;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=J138;

RX MEDLINE=20330349; PubMed=10871362;

RA Shiba T., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138

RL from Japan and CWL029 from USA.";

RL Nucleic Acids Res. 28:2311-2314 (2000).

DR BMBL; AP002545; BAA98227.1; -

DR InterPro; IPR003368; Chlamydia_PMP.

DR Pfam; PF02415; DUF145; 1.

DR TIGRFAMs; TIGR01376; POMP_repeat; 6.

SQ SEQUENCE 427 AA; 43419 MW; AB4BBBCL594DD2B1 CRC64;

Alignment Scores:

Pred. No.: 1,35e-38 Length: 427

Score: 792.00 Matches: 198

Percent Similarity: 59.56% Conservative: 70

Best Local Similarity: 44.00% Mismatches: 146

Query Match: 14.64% Indels: 36

DB: 16 Gaps: 14

US-09-428-122-1 (1-3000) x Q9RB70 (1-427)

Qy 101 ATGAAGTCTTCTTCCCAAGTTGTATTTTCTACATTGCTATTTTCCCTTTGCTCTATG 160

Db 1 MetArgSerSerPheSerLeuLeuLeuLeuSerSerSerLeuAlaPheProLeuLeuMet 20

Qy 161 ATT-----GCTACCGAGACAGTTTTCGATTTCAGTTCGAGTTCGAGTTCGGAAT 208

Db 21 SerValSerAlaAspAlaAlaAspLeuThrLeuGlySerArgAspSerTyrAsnGlyAsp 40
QY 209 ---AAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACCTAC 262
Db 41 ThrSerThrThrGluPheThrProLysAlaAlaThrSerAspAlaSerGlyThrThrTyr 60
QY 263 CTATTATAGGGAATGTCACCTAGAAATATCTCTGGAACAGGACACAGCAATACAAAA 322
Db 61 IleLeuAspGlyAspValSerIleSerGln---AlaGlyLysGlnThrSerLeuThrThr 79
QY 323 AGCTGTTTAAACAACACTAAGGCCATTTGACTTTTCACAGGTAAACGGGAATCTCTATTG 382
Db 80 SerCysPheSerAsnThrAlaGlyAsnLeuThrPheLeuGlyAsnGlyPheSerLeuHis 99
QY 383 TTCAAAACGGTGGATGCGAGGACTGTAGAGGGGCTGCTGTAAACAGCAGCGGTGTAGAT 442
Db 100 PheAspAsnIleSerThrValAlaGlyValValSerAsnThrAlaAlaSer 119
QY 443 AAATCTACACGCTTTATAGGTTTCTTCGCTATCTTTTATTCGCTCTCTCGGAAGTTTCG 502
Db 120 GlyIleThrLysPheSerGlyPheSerThrLeuArgMetLeuAlaAlaProArg----- 137
QY 503 ATAACTACCGCAAGAGCCCTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAAAT 562
Db 138 ---ThrThrGlyLysGlyAlaIleLysIleThrAspGly---LeuValPheGluSerIle 155
QY 563 GTCAGTTTCTCTCAGCAAAACCTTTCAACGGATATATGGGGTGTCTATCACCCAAAA 622
Db 156 GlyAsnLeuAspLeuAsnGluAsnAlaSerSerGluAsnGlyGlyAlaIleAsnThrLys 175
QY 623 ACTCTTTTCATTAACAGGAGTACAAATGTCAGCTCTGTTTCTGAAAATACCTCTCAAG 682
Db 176 ThrLeuSerLeuThrGlySerThrArgPheValAlaPheLeuGlyAsnSerSerGln 195
QY 683 AAAGCGGAGCCATTCAGACTTCGATGCCCTTACCATTTACTGTGAAACCAAGGGAGTC 742
Db 196 GlnGlyGlyAlaIleTyrAlaSerGlyAspSerValIleSerGluAsnAlaGlyIleLeu 215
QY 743 TCTTTTCTGCAATACCTCTTCGGATTCGTGAGCTGCAATTTTACAGAACCTCGGTG 802
Db 216 SerPheGlyAsnAsnSerAlaThrThrSerGlyGlyAlaIleSerAlaGluGlyAsnLeu 235
QY 803 ACTATTCTAATAATGCTAAAGTTCTTATTTATGCAATAGGTCACAGGACGAGCTCC 862
Db 236 ValIleSerAsnAsnGlnAsnIlePhePheAspGlyCysLysAlaThr----- 251
QY 863 TCAACAACGGGGATATGTCAGGAGTGTCTATCTGTCTTATAAA-----ACTAGTACA 916
Db 252 -----ThrAsnGlyGlyAlaIleAspCysAsnLysAlaGlyAlaAsnPro 266
QY 917 GATCTAAGGTCACTCGAATCAGATGTTACTCTTCAGCAACAAATACATCGACA 976
Db 267 AspProIleLeuThrLeuSerGlyAsnGluSerLeuHisPheLeuAsnAsnThrAlaGly 286
QY 977 ACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGCTCCGGA---GGACTACC 1033
Db 287 AsnSerGlyGlyAlaIleTyrThrLysLysLeuValLeuSerSerGlyArgGlyVal 306
QY 1034 CTATTCTAGTAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATC 1093
Db 307 LeuPheSerAsnAsnLysAlaAlaAsnAlaThr---ProLysGlyGlyAlaIleAlaIle 325
QY 1094 GAAGATAGTGGGAATGATTTATCCGCCGATAGTGGTGACATTCCTCTTTTAGGGAAT 1153
Db 326 LeuAspSerGlyGluIleSerIleSerAlaAspLeuGlyAsnIleIlePheGluGlyAsn 345
QY 1154 ACAGTCACTCTCTACTACT-----CCTGGGACCAATAGATAGTATCGACTTAGGA 1204
Db 346 Thr---ThrSerThrThrGlySerProAlaSerValThrArgAsnAlaIleAspLeuAla 364
QY 1205 ACGAGTCAAGATGACAGCTTTGCGTTCTGCTGCTGTAGAGCCATCTACTTCTATGAT 1264
Db 365 SerAsnAlaLysPheLeuAsnLeuArgAlaThrArgGlyAsnLysValIlePheTyrAsp 384

QY 1265 CCCATTACTACAGGATCATCCACACAGTTACAGATGCTCTAAAGTTAATGAGACTCCG 1324
Db 385 ProfileThr-----SerSerGlyAlaThrAspLysLeuSerLeuAsnLysAlaAsp 401
QY 1325 GCAGATTCTGCACCTACAAATATACAGGGAACATCATCTTTCACAGGAGAAAAGTTATCAGAG 1384
Db 402 AlaGlySerGlyAsnThrTyrTyrGluGlyTyrIleValPheSerGlyGluLysLeuSerGlu 421
QY 1385 ACAGAGGCGGACAGATTCTTAAAAATCTTACT 1414
Db 422 Val-----ArgAsnLeuThr 426

Search completed: December 16, 2003, 10:27:47
Job time : 168.5 secs

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OM protein - protein search, using sw model

Run on: December 16, 2003, 10:33:19 ; Search time 47 seconds
(without alignments)
3134.006 Million cell updates/sec

Title: US-09-428-122-2
Perfect score: 4774
Sequence: 1 MKSFPKVFSTFAIFPLSM.....FELKSSRNYNVDLAKYQF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4774	100.0	928	21	AA194327
2	4760	99.7	928	20	AAW88421
3	3865	81.0	746	23	ABB90535
4	2802.5	58.7	597	20	AA194611
5	2058	43.1	928	20	AAW88418
6	2048	42.9	928	23	ABB90573
7	2021	42.3	928	21	AA190237
8	2006	42.0	918	21	AA196274
9	2001	41.9	918	20	AAW88422

10	1993	41.7	914	20	AAW88429	Chlamydia pneumoni
11	1987.5	41.6	895	21	AA190238	Mature Chlamydia a
12	1986	41.6	928	20	AAW88423	Chlamydia pneumoni
13	1982	41.5	928	23	ABB90542	Chlamydia pneumoni
14	1976	41.4	928	21	AA190239	Chlamydia antigen
15	1965	41.2	936	21	AA199842	Chlamydia pneumoni
16	1965	41.2	936	21	ABB90602	Chlamydia pneumoni
17	1946.5	40.8	925	21	AA199843	Chlamydia pneumoni
18	1940	40.6	930	20	AA1935052	Chlamydia pneumoni
19	1936	40.6	930	23	ABB90548	Chlamydia antigen
20	1930	40.4	930	21	AA190240	Chlamydia pneumoni
21	1927	40.4	930	20	AAW88424	Chlamydia pneumoni
22	1917.5	40.2	927	20	AA1935054	Chlamydia pneumoni
23	1915	40.1	926	23	ABP56019	Chlamydia psittaci
24	1915	40.1	926	23	ABB98228	Chlamydia psittaci
25	1915	40.1	926	24	ABU66284	C. psittaci protei
26	1856	38.9	949	20	AA1935060	Chlamydia pneumoni
27	1855	38.9	928	20	AAW88417	Chlamydia antigen
28	1855	38.9	928	21	AA190236	Chlamydia pneumoni
29	1855	38.9	928	23	ABB90583	Amino acid sequenc
30	1832	38.4	945	21	AA193358	Chlamydia pneumoni
31	1811	37.9	945	20	AAW88428	Chlamydia psittaci
32	1656.5	34.7	839	23	ABP56002	Chlamydia polypept
33	1656.5	34.7	839	23	ABB98211	C. psittaci protei
34	1656.5	34.7	839	24	ABU66267	Chlamydia pneumoni
35	1573	32.9	841	23	ABB90595	Chlamydia pneumoni
36	1572.5	32.9	643	20	AA1935056	C. pneumoni
37	1570	32.9	841	21	AA192818	Chlamydia pneumoni
38	1564	32.8	841	20	AAW88420	Chlamydia pneumoni
39	1442.5	30.2	922	23	ABB90546	Chlamydia pneumoni
40	1437.5	30.1	922	21	AA195548	Chlamydia pneumoni
41	1430.5	30.0	922	20	AAW88419	Chlamydia pneumoni
42	1417.5	29.7	922	20	AA194597	Chlamydia pneumoni
43	1383.5	29.0	1407	23	ABB90541	Chlamydia pneumoni
44	1377.5	28.9	973	21	AA196274	Chlamydia POMP91B
45	1377.5	28.9	973	23	ABB90527	Chlamydia pneumoni

ALIGNMENTS

RESULT 1
AA194327
ID AA194327 standard; Protein; 928 AA.
XX
AC AA194327;
XX
DT 11-AUG-2000 (first entry)
XX
DE Chlamydia pneumoniae 98kD putative outer membrane protein.
XX
KW Chlamydia; antigen; vaccine; infection; outer membrane protein.
XX
OS Chlamydia pneumoniae.
XX
PN WO200026237-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-GB03579.
XX
PR 29-OCT-1998; 98US-0106070.
PR 01-MAR-1999; 99US-0122066.
PR 27-OCT-1999; 99US-0428122.
XX
(CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Dunn PL;
XX
XX WPI; 2000-365569/31.
DR N-PSDB; AAA27021.
XX
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used

PT for vaccination and protection against Chlamydia infection

PS Claim 6; Fig 1; 93pp; English.

XX The present sequence is the 98kDa putative outer membrane protein from
CC Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BglI restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamHI and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The present polypeptide may also be administered orally to treat
CC Chlamydia infection.

XX Sequence 928 AA;

Query Match 100.0%; Score 4774; DB 21; Length 928;

Best Local Similarity 100.0%; Pred. No. 6.5e-305;

Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKSSFPKVFSTFAIPPLSMIATETVLDSSAGFDGKNGNFSVRESQEDAGTTLFKGNV	60
Db	1	MKSSFPKVFSTFAIPPLSMIATETVLDSSAGFDGKNGNFSVRESQEDAGTTLFKGNV	60
QY	61	TLENIPGTGTATKSCFNNTKGLTFTGNGSNLLFQTVDAAGTVAGAAVNSVVDKSTTFI	120
Db	61	TLENIPGTGTATKSCFNNTKGLTFTGNGSNLLFQTVDAAGTVAGAAVNSVVDKSTTFI	120
QY	121	GRSSLSFIAPSGSIITTGKAVSCSTGSLSTKNVLLFSKNFSTPDGGAITAKTLLSLG	180
Db	121	GRSSLSFIAPSGSIITTGKAVSCSTGSLSTKNVLLFSKNFSTPDGGAITAKTLLSLG	180
QY	181	TTMSALFSENTSSKKGAIQTSALITNGQGVSPSDNTSSDGAIAIFTEASVTISNNA	240
Db	181	TTMSALFSENTSSKKGAIQTSALITNGQGVSPSDNTSSDGAIAIFTEASVTISNNA	240
QY	241	KVSFIDNKVTGASSITTGDMSGGAI CA YKTSTDTKVTLTGNOMLLFSNNTSTTAGAIYV	300
Db	241	KVSFIDNKVTGASSITTGDMSGGAI CA YKTSTDTKVTLTGNOMLLFSNNTSTTAGAIYV	300
QY	301	KLELASGGLTFSRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSTPGT	360
Db	301	KLELASGGLTFSRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSTPGT	360
QY	361	NRSSIDLGTSAKMTALRSAGRAIYFVDPITTGSSITVTDLKVNTPADSALQYTGNI	420
Db	361	NRSSIDLGTSAKMTALRSAGRAIYFVDPITTGSSITVTDLKVNTPADSALQYTGNI	420
QY	421	FTGEKLSSETAADSKNLTSLKLOPVTLSSGGLTSLKHGVTIQTQAFQOADSRLMDVGT	480
Db	421	FTGEKLSSETAADSKNLTSLKLOPVTLSSGGLTSLKHGVTIQTQAFQOADSRLMDVGT	480
QY	481	LEPADTGTINNLVINISIDGAKKAKIETKATSKNLTLSGTITILLDPTGTFYENHSRLNP	540
Db	481	LEPADTGTINNLVINISIDGAKKAKIETKATSKNLTLSGTITILLDPTGTFYENHSRLNP	540
QY	541	QSYDILELKASGTVTSTAVTDDPIMGEKPHYGYGTGWPVIMVGTGASTTATFNWTKGYI	600
Db	541	QSYDILELKASGTVTSTAVTDDPIMGEKPHYGYGTGWPVIMVGTGASTTATFNWTKGYI	600
QY	601	PNPERIGSLVNSLWNAFIDISLHYLMETANEGLOGDRAFCWAGLNFHFKDSTKTRRG	660
Db	601	PNPERIGSLVNSLWNAFIDISLHYLMETANEGLOGDRAFCWAGLNFHFKDSTKTRRG	660

QY	661	FRHLSGGYVIGGNLHTCSDKILSAAFCQLFRDRDYFAKNQGTYYGGLYYQHNETYIS	720
Db	661	FRHLSGGYVIGGNLHTCSDKILSAAFCQLFRDRDYFAKNQGTYYGGLYYQHNETYIS	720
QY	721	LPCKLRPCSLSYVTEIPVLPSGNLSYTHTDNDLTKYTTYPTVKGSGWGNDSFALEFGGR	780
Db	721	LPCKLRPCSLSYVTEIPVLPSGNLSYTHTDNDLTKYTTYPTVKGSGWGNDSFALEFGGR	780
QY	781	APICLDESALFEQYMPFMKIQFYVAHQEGFKQTEAREFGSSRLVNLALPIGIRFDKES	840
Db	781	APICLDESALFEQYMPFMKIQFYVAHQEGFKQTEAREFGSSRLVNLALPIGIRFDKES	840
QY	841	DCQDATYNLTIGYTVDLVRSNPDCTTTLRISGDSWKTEGTLARQALVLRAGNHPCFNSN	900
Db	841	DCQDATYNLTIGYTVDLVRSNPDCTTTLRISGDSWKTEGTLARQALVLRAGNHPCFNSN	900
QY	901	FEAFSQSFELRGSSRNYNVDLGAQYQF	928
Db	901	FEAFSQSFELRGSSRNYNVDLGAQYQF	928

RESULT 2

AAW88421

ID AAW88421 standard; Protein; 928 AA.

XX AAW88421;

XX 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp8.

XX Omp8; outer membrane protein 8; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydia pneumoniae.

XX WO958953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-DK00266.

XX 23-JUN-1997; 97DK-0000744.

XX (BIRK/) BIRKELUND S.

XX (CHRI/) CHRISTIANSEN G.

XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
XX Mygind P;

XX WPI; 1999-105610/09.

XX N-PSDB; AAX06820.

XX Species-specific test for identifying mammals infected with
XX Chlamydia pneumoniae - comprises detecting antibodies specific for
XX outer membrane proteins of C. pneumoniae or nucleic acids encoding
XX these proteins

XX Claim 7; Page 53-55; 115pp; English.

XX This polypeptide comprises the novel 90.0 kDa surface exposed
XX protein Omp8 of the human respiratory pathogen Chlamydia
XX pneumoniae. Its amino acid sequence was deduced from DNA (see
XX AAX06820) isolated from a C. pneumoniae expression library. The
XX invention provides 12 novel surface exposed proteins, Omp4-Omp15
XX (see AAW88417-28), and nucleic acid sequences encoding them (see
XX AAX06816-27). A new species specific test is claimed that is used
XX to identify mammals (including humans) infected with Chlamydia
XX pneumoniae. The test comprises detecting antibodies specific for
XX Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
XX membrane proteins, especially by PCR. The proteins are also used
XX in the diagnosis of C. pneumoniae infection in mammals. The

CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma.
CC which are possibly associated with C. pneumoniae.
XX
SQ Sequence 928 AA;
Query Match 99.7%; Score 4760; DB 20; Length 928;
Best Local Similarity 99.7%; Pred. No. 5.4e-304;
Matches 925; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKSFPKVFSTFAIFPLSMIATETVLDSSASFGKNGNPFVRESQEDAGTTLFKGNV 60
DB 1 MKSFPKVFSTFAIFPLSMIATETVLDSSASFGKNGNPFVRESQEDAGTTLFKGNV 60
QY 61 TLENIPTGTATITKSCFNNTKGDITFTGNGSLLFQTVDACTVAGAAVNSVVDKSTTFI 120
DB 61 TLENIPTGTATITKSCFNNTKGDITFTGNGSLLFQTVDACTVAGAAVNSVVDKSTTFI 120
QY 121 GFSLSFIASPGSSITTKGAVSCSTGSLSTKXVSLLFKNFSTNDNGCAITAKTSLTGT 180
DB 121 GFSLSFIASPGSSITTKGAVSCSTGSLKFKDKVSLLFKNFSTNDNGCAITAKTSLTGT 180
QY 181 TTMSALFSENTSSKKGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 240
DB 181 TTMSALFSENTSSKKGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 240
QY 241 KVSFIDNKVTGASSTTGDMSGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 300
DB 241 KVSFIDNKVTGASSTTGDMSGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 300
QY 301 KKLKELASGGLTLTFRNSVNGGTAPKGGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 360
DB 301 KKLKELASGGLTLTFRNSVNGGTAPKGGAIQTSALTITGNGEVSFSDNTSSDGAIIFTASVTISNNA 360
QY 361 NRSSIDLGTSAKWTALRSAGRAIYFDPITGSSSTTVTDVLKVNETPADSALQYTGNI 420
DB 361 NRSSIDLGTSAKWTALRSAGRAIYFDPITGSSSTTVTDVLKVNETPADSALQYTGNI 420
QY 421 FTGKELSETEADSKNLSKLLQPTVLSGGLTSLKHGVTLOQAFQQAQDSLEMDVGT 480
DB 421 FTGKELSETEADSKNLSKLLQPTVLSGGLTSLKHGVTLOQAFQQAQDSLEMDVGT 480
QY 481 LEPADTSTNNLVINISSIDGAKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 540
DB 481 LEPADTSTNNLVINISSIDGAKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 540
QY 541 QSYDILELAKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGASTTATFNWTKGYI 600
DB 541 QSYDILELAKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGASTTATFNWTKGYI 600
QY 601 PNPRIKSLVPSNLWAFIDISLHLYMETANEGLOGDRAFCAGISNPFHKDSTKTRRG 660
DB 601 PNPRIKSLVPSNLWAFIDISLHLYMETANEGLOGDRAFCAGISNPFHKDSTKTRRG 660
QY 661 FRHLGGYVIGGNLHSCDKILSAFCOLFGRDRDYFAKNQGTGVYGGTLYYQHNETYIS 720
DB 661 FRHLGGYVIGGNLHSCDKILSAFCOLFGRDRDYFAKNQGTGVYGGTLYYQHNETYIS 720
QY 721 LPCKLRPCSLSYVPTETPVLPSGNLSYTHTDNLDLTKYTTYPTVKGSGWNSDPALEFGGR 780
DB 721 LPCKLRPCSLSYVPTETPVLPSGNLSYTHTDNLDLTKYTTYPTVKGSGWNSDPALEFGGR 780
QY 781 APICLDESALFEQMPMKLOFYVAHQEGKEQTEAREFGSSRLVNLALPIGIRFDKES 840
DB 781 APICLDESALFEQMPMKLOFYVAHQEGKEQTEAREFGSSRLVNLALPIGIRFDKES 840
QY 841 DCQDATYNTLGYTVDLVRNPDCTTLTIRISGDSWKTFGTNLARQALVLRAGNHFCEFSN 900
DB 841 DCQDATYNTLGYTVDLVRNPDCTTLTIRISGDSWKTFGTNLARQALVLRAGNHFCEFSN 900
QY 901 FEAFSQFSFELRGSSRNYNVDLCAKYQF 928

DB 901 FEAFSQFSFELRGSSRNYNVDLCAKYQF 928
RESULT 3
ABB90535
ID ABB90535 standard; Protein; 746 AA.
XX ABB90535;
AC ABB90535;
XX 29-JUL-2002 (first entry)
DT 29-JUL-2002 (first entry)
XX Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.
DE Chlamydia pneumoniae; antigen; immunogen; vaccine; diagnosis;
XX human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
XX strain CWL029.
OS Chlamydia pneumoniae.
XX WO200202606-A2.
XX 10-JAN-2002.
XX 03-JUL-2001; 2001WO-IB01445.
XX 03-JUL-2000; 2000GB-0016363.
PR 11-JUL-2000; 2000GB-0017047.
PR 21-JUL-2000; 2000GB-0017983.
PR 07-AUG-2000; 2000GB-0019368.
PR 18-AUG-2000; 2000GB-0020440.
PR 14-SEP-2000; 2000GB-0022583.
PR 10-NOV-2000; 2000GB-0027549.
PR 22-DEC-2000; 2000GB-0031706.
XX (CHIR-) CHIRON SPA.
XX Ratti G, Grandi G;
XX WPI; 2002-154726/20.
DR N-PSDB; ABL91193.
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX Claim 1; Page 49-50; 364pp; English.
PS Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
XX pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.
XX
SQ Sequence 746 AA;
Query Match 81.0%; Score 3865; DB 23; Length 746;
Best Local Similarity 100.0%; Pred. No. 2.5e-245;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	183	MSALFSENTSSKKGAIQTSDALTIITGNOGEVSFSDNTSSDGAAIPTFEASVTISNNAKV	242
Db	1	MSALFSENTSSKKGAIQTSDALTIITGNOGEVSFSDNTSSDGAAIPTFEASVTISNNAKV	60
QY	243	SFIDNKVTGASSSTTGMDSGGAICAYKTSTDTKVTITGNQMLLFSNNSTSTAGGAIYVKK	302
Db	61	SFIDNKVTGASSSTTGMDSGGAICAYKTSTDTKVTITGNQMLLFSNNSTSTAGGAIYVKK	120
QY	303	LELASGGTLFSRNSVNGGTAPKGAITAIEDSGELSLSAOSGDIVFLGNTVTSITPGTNR	362
Db	121	LELASGGTLFSRNSVNGGTAPKGAITAIEDSGELSLSAOSGDIVFLGNTVTSITPGTNR	180
QY	363	SSIDLGTSAKMTALRSAAGRAIFYDPIITGSSSTVTDVLKVNETPADSALOYTGNIIFT	422
Db	181	SSIDLGTSAKMTALRSAAGRAIFYDPIITGSSSTVTDVLKVNETPADSALOYTGNIIFT	240
QY	423	GEKLSETAADSKNLTSKLLQPVTLISGGTSLSKHGVTLOTAFTQOADSRLMDVGTILE	482
Db	241	GEKLSETAADSKNLTSKLLQPVTLISGGTSLSKHGVTLOTAFTQOADSRLMDVGTILE	300
QY	483	PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQS	542
Db	301	PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNPQS	360
QY	543	YDILBKASGVTSTAVTPDPIMGSKPHYGQGTWGPVWGTGASTTATFNWTKGYIPN	602
Db	361	YDILBKASGVTSTAVTPDPIMGSKPHYGQGTWGPVWGTGASTTATFNWTKGYIPN	420
QY	603	PERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFCWAGLSNFFHKDSTKTRGRFR	662
Db	421	PERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFCWAGLSNFFHKDSTKTRGRFR	480
QY	663	HLSGGVYVIGGNLHTCSDKILSAACQLFGRDRDYFVAKNQGTVYGGLTYOHNETYISLP	722
Db	481	HLSGGVYVIGGNLHTCSDKILSAACQLFGRDRDYFVAKNQGTVYGGLTYOHNETYISLP	540
QY	723	CKLRPCSLSYVTEIPVLFSGNLSYTHTDNLTKVTTYPTVYKSGMGNDSFALEFGGRAP	782
Db	541	CKLRPCSLSYVTEIPVLFSGNLSYTHTDNLTKVTTYPTVYKSGMGNDSFALEFGGRAP	600
QY	783	ICLDESALFEQYMPFMKLOFVYAHQBGFEQGTGEAREFGSSRLVNLALPIGIRFDFKESDC	842
Db	601	ICLDESALFEQYMPFMKLOFVYAHQBGFEQGTGEAREFGSSRLVNLALPIGIRFDFKESDC	660
QY	843	QDATYNLTIGYTVDLVRSNPDCCTTILIRISGDSWKTEFTGNLARQALVLRAGNHFCFNSNFE	902
Db	661	QDATYNLTIGYTVDLVRSNPDCCTTILIRISGDSWKTEFTGNLARQALVLRAGNHFCFNSNFE	720
QY	903	AFSOFSEFLRGSRRNNVDLGAKYQF	928
Db	721	AFSOFSEFLRGSRRNNVDLGAKYQF	746

RESULT 4	
AAAY34611	
ID	AAAY34611 standard; Protein; 597 AA.
XX	
XX	AAAY34611;
XX	AC
XX	XX
DT	13-SEP-1999 (first entry)
XX	
DE	Chlamydia pneumoniae transmembrane protein sequence.
XX	
KW	Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW	sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW	vaccine; neutralising epitope.
XX	
OS	Chlamydia pneumoniae.
XX	
XX	WO9927105-A2.
FN	
XX	
XX	03-JUN-1999.
PD	
XX	

PF	20-NOV-1998;	98WO-1B01890.	
XX			
PR	04-NOV-1998;	98US-0107078.	
PR	21-NOV-1997;	97FR-0014673.	
XX			
XX	(GEST) GENSET.		
PA			
XX			
PI	Griffais R;		
XX			
DR	WPI; 1999-357842/30.		
XX			
PT	Genome sequence of Chlamydia pneumoniae		
XX			
PS	Page 632-633; Disclosure; 1912pp; English.		
XX			
CC	AAV34584-Y35879 represent the proteins encoded by all the open reading		
CC	frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.		
CC	C. pneumoniae causes respiratory disease such as pneumonia and		
CC	bronchitis and is thought to be a contributing factor in heart		
CC	disease, sarcoidosis, sinusitis, purulent otitis media, erythema		
CC	nodosum or pharyngitis. The polypeptides encoded by the open reading		
CC	frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in		
CC	immunogenic compositions as vaccines. Vectors containing C. pneumoniae		
CC	nucleotides sequences can also be used as immunogenic compositions,		
CC	especially where the vector directs the expression of a neutralising		
CC	epitope of C. pneumoniae.		
XX			
XX	Sequence 597 AA;		
SQ			
Query Match 58.7%; Score 2802.5; DB 20; Length 597;			
Best Local Similarity 93.8%; Pred. NO. 1.2e-175;			
Matches 560; Conservative 5; Mismatches 21; Indels 11; Gaps 3;			

Qy		149	LSLTKVNSLLFSKNFSTDNCGAIIAKTILSUTGTTMSALFSENNTSKKGAIGQTSDALIIT	208
Db		1	LEFDKNYSLLFSKNFSTDNCGAIIAKTILSUTGTTMSALFSENNTSKKGAIGQTSDALIIT	60
Qy		209	GNOGEVSFNNTSSDSGAALFTESAVTIISNNAKVSIDNKVTGCASSSTTGDMSGCAICAY	268
Db		61	GNOGEVSFNNTSSDSGAALFTESAVTIISNNAKVSIDNKVTGCASSSTTGDMSGCAICAY	120
Qy		269	KTSJDTKVTLTGOMQLFPSNNTSTTAGGAIYVKKLELASGGLTFSRNSVNGGTAPKGGA	328
Db		121	KTSJDTKVTLTGOMQLFPSNNTSTTAGGAIYVKKLELASGGLTFSRNSVNGGTAPKGGA	180
Qy		329	IAIEDSGELSADSGBDIVLGNVTYSTPGRNRSSIDIGTSAKMTALBSAGRAIIFYD	388
Db		181	IAIEDSGELSADSGBDIVLGNVTYSTPGRNRSSIDIGTSAKMTALBSAGRAIIFYD	240
Qy		389	PITTGSSSTTVTDVLKVNETPADSALOYTGNIIPTGKELSEADSKNLTSKLLQPVTLS	448
Db		241	PITTGSSSTTVTDVLKVNETPADSALOYTGNIIPTGKELSEADSKNLTSKLLQPVTLS	300
Qy		449	GGTLSLKHGVTLQTAFTQQADSRLEMVDGTTLEPPADTSTINNLVINISIDGAKKAIE	508
Db		301	GGTLSLKHGVTLQTAFTQQADSRLEMVDGTTLEPPADTSTINNLVINISIDGAKKAIE	360
Qy		509	TKATSKNLTLSGTTILDPTGTFYENHSLRNPQSYDILELKASGTTVSTAVTPDDTWGEK	568
Db		361	TKATSKNLTLSGTTILDPTGTFYENHSLRNPQSYDILELKASGTTVSTAVTPDDTWGEK	420
Qy		569	FHYGYOQTGWPIVMWGTGASTTATFNWTKTGYIPNPERIGSLVPNSLNWNAFIDISSLHLYM	628
Db		421	FHYGYOQTGWPIVMWGTGASTTATFNWTKTGYIPNPERIGSLVPNSLNWNAFIDISSLHLYM	480
Qy		629	ETANEGLODRAFWCAGLSNFPHXKOSTKRGRPFHLSGGVYVIGNLHTCSDKILSAFCQ	688
Db		481	ETANEGLODRAFWCAGLSNFPHXKOSTKRGRPFHLSGGVYVIGNLHTCSDKILSAFCQ	540
Qy		689	LFGRDRDYFAKNQG-ITYYGCTLYYQHNETVIS-----LPCKLR+PCSLSYYP	734
Db		541	LFGRDRDYFAKNORYSLRRNSLPAQRNULSSLOQTALFWVLVCSDSVRDCSLFRKP	597

Db 116 NLSLTGFFSLTFLAAPSIVITPSGKGVKCG-GDLTFDNNGTILFKQDYCEENGGAIST 174
Qy 174 KTLISLTGTTMSALFSENSTSS--KKGAIQTSDALITTCNQGEVFSFSDNTSSDGAIAFT 230
Db 175 KNLSLKNSGTSISFEGNKSATKGGGAI CATGTVDITNTAPTLESNNIAAAGGAINS 234
Qy 231 EASVTISNNAKVSFIDNKVTGASSSTGDMGGAICAYKTSTDTKVTLLTGNNQMLFNSNT 290
Db 235 TGNCTTGTNTSLVSENSVT----ATAG--NGGAL-----SGDADVTISGNQSVTFSGNQ 283
Qy 291 STTAGGAIYKKLELAS--GGLTLFSRNSVNGTAPKGGAIATEDSGELSLSDSDIYF 348
Db 284 AVANGGAIYAKKLTLAGGGGGISFNNIVQGTAGNGGAISILAAEGCSLSAEGDIIF 343
Qy 349 LGNTVSTTP-GNRRSIDLGTAKMTALRSAGRAIYFYDPTITGSSSTVTVDLVKXNET 407
Db 344 NGNAIVATTPTQTKRNSIDIGSTAKTNLRAISGHSIFFYDPTITANTAADSTDTLNKA 403
Qy 408 PADSALOYTGNIIFTGKLESETAADSKNLTSKLLQPVLSGGTSLKKGVTTLQTAFTQ 457
Db 404 DAGNSTDYSGSIVFSGEKLSEDAKVADNLTSTLKQPVTLTAGNLVLRGVTLDTKGFTQ 463
Qy 468 QADSRLEMDVGTILEPA-DTSTINNLVINISSIDGAKAKIETKATSKNLTLTSGTITLLD 526
Db 464 TAGSSVIMDAGTTKASTEEVTLTGLSIPVDSLGEKKVIVIAASAASKNVALSGPILLDD 523
Qy 527 PTGTFYENHSLRNQPSQDILELKASGTVTGTAVTPDPIMGKPHYGYQGTWGPVW---- 582
Db 524 NQWAYENHDLGKTQDFSVQLSALGTATTVDVPAVTPVATPHYGYQGTWGW-MTWVDDT 582
Qy 583 -GTGAATTATFNWTKTYIIPNERIGSLVPNSLWNAFIDISLHLMETANEGLOGDRAF 641
Db 583 ASTEPTKTATLAWNTGYLPNPGRQGPLVNSLWMSFSDIAIQGVVERSALTLCSDRGF 642
Qy 642 WCAGLSNPFHKDSTKTRGRFHLGGVYVGNLHCTCDKILSAFCOLFGRDRDYFAKN 701
Db 643 WAAGVANFLDKDKKGEKRYHKSGGYAGGAAGTCSNLIISFAFQCLFGSDDKDLVAKN 702
Qy 702 QGTVYGTLVYQHNETVSLPCKLRPCSLSVYP--TEIPVLFSGNISYTHTDNDLTKY 758
Db 703 HTDYAGAFYIQH-----ITECSGFIGCLLDKLPQSWSHKPLVLGQLAYSHVNDLTKY 758
Qy 759 TTYPTVKGWGNDSFALFEGGRAPICLDESALFPQYMPFMKLFQVYAHQEGFKQGTAR 818
Db 759 TAYPEVKGWGNNAFNMMLGASSHSYPEYLHCFDTYAPYIKLNTYIRQDSFSEKGTGR 818
Qy 819 EFGSSRLVNLALPTGIRFKESDCODATYNTLGTVDLRSNPDCTTLIRISGDSWKTF 878
Db 819 SFDDSNLFLSLPIGVKPEKFCDCNDFSYDITLSTVYDPLIRNDPKCITLALVISASWET 878
Qy 879 GTNLARQALVLRAGNHFCFNSNFAPFSQFSELRGS 914
Db 879 ANNARQALQVRAGSHYAFSPMFEVLGQFVEVRGS 914

RESULT 11

AAAY90238

ID AAAY90238 standard; Protein; 885 AA.

XX AAAY90238;

AC AAAY90238;

XX 29-AUG-2000 (first entry)

XX Mature Chlamydia antigen CPN100635.

DE Chlamydia antigen; diagnosis; infection; community acquired pneumonia;

XX therapy; upper respiratory tract disease; bronchitis; sinusitis;

KW asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.

OS Chlamydia pneumoniae.

XX WO200032794-A2.

PN

XX 08-JUN-2000.
XX 01-DEC-1999; 9990-CA01147.
XX 01-DEC-1998; 98US-0110339.
XX 01-DEC-1998; 98US-0110340.
XX 01-DEC-1998; 98US-0110427.
XX 01-DEC-1998; 98US-0110428.
XX 01-DEC-1998; 98US-0110438.
XX (CONN-) CONNAUGHT LAB LTD.
XX Murdin AD, Omen RP, Wang J;
XX WPI; 2000-412339/35.
XX N-PSDB; AAA30849, AAA30850.
XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset asthma -
XX Claim 16; Fig 3; 174pp; English.
XX This sequence is a Chlamydia antigen of the invention, designated CPN100635. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of disease (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults.

XX Sequence 885 AA;

Query Match 41.6%; Score 1987.5; DB 21; Length 885;
Best Local Similarity 46.9%; Pred. No. 7.6e-122;
Matches 420; Conservative 136; Mismatches 302; Indels 37; Gaps 16;

Qy 51 GTTYLPKGNVTLENIPTGTATKSCFNNTKGDLTFTGNGNSLLFQTVDA GTVAGAAVNS 110
Db 11 GIDYTLTGDTLQML-GDSALTKGCFSDTTESLFPAGKGYSLFLNKS-SABGAAL-S 67
Qy 111 SVVDKSTTFIGFSSLSFIASPGSSITT--GKGA VSCSTGSLSTKTVLSLFSKNTFSDNG 168
Db 68 VTTDKNLSLGTGFFSLTFLAAPSSVITTPSGKGVKCG-GDLTFDNNGTILFKQDYCEENG 126
Qy 169 GAITAKTLSLTGTTMSALFSENSTSS---KKGAIQTSDALITTCNQGEVFSFSDNTSSDSG 225
Db 127 GAISTKNLSLKNSTGTSISFEGNKS SATKKGGAICATGTVDITNTAPTLESNNIAAAG 186
Qy 226 AAIFTEASVTISNNAKVSFIDNKVTGASSSTGDMGGAICAYKTSTDTKVTLLTGNNQML 285
Db 187 GAINSTGNTCTTGTNTSLVSENSVT----ATAG--NGGAL-----SGDADVTISGNQSVT 235
Qy 286 FSNNTSTTAGGAIYKKLELAS--GGLTLFSRNSVNGTAPKGGAIATEDSGELSLSDS 343
Db 236 FSGNQAVANGGAIYAKKLTLAGGGGGISFNNIVQGTAGNGGAISILAAEGCSLSFSEA 295
Qy 344 GDIVFLGNVTSTTP-GTNRSSIDLGTSAKMTALRSAGRAIYFYDPTITGSSSTVTVDLV 402
Db 296 GDHYLNGNAIVATTPTQTKRNSIDIGSTGDKDHLRAISGHSIFFYDPTITANTAADSTDTL 355

Db 645 EGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNLITAAFCQLFGKORDHFINKRA 704
Qy 704 TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLSGNLSYTHTDNDLTKYTT 760
Db 705 SAYAASLHLQHLATLSS-----PSLLRYLPSSESEQPVLPFAQISYIYKNTMYTYTQ 758
Qy 761 YPTVKGWGNDSFALEFGGRAP-ICLDESALFEQYMPFMKLOFYVAHQSGFKQGTG-AR 818
Db 759 APKGSSWYNDGCALELASSLPHTALSHEGLFHAFFIKVEASYIHQDSFKERNITLVR 818
Qy 819 EFGSSRLVNLALPIGRFKESQCDATNLTGTYVDLVRSPDCCTTLRISGSKWTF 878
Db 819 SFDSGDLINVSFVIGHTFFERSNERASYEATVIYVADYVRKNPDCTTALLINNTSWKTT 878
Qy 879 GTNLARQALVLRAGNHFCSNFEAFSQFSFELRGSSRNYNVDLGAQYOF 928
Db 879 GTNLSRQAGIGRAGIFYAFSPNLEVTNLSMEIRGSSRSYNADLGKQFQF 928

RESULT 13

ABB90542
ID ABB90542 standard; Protein; 928 AA.

AC ABB90542;

XX 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp6731 protein, SEQ ID NO:33.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029.

XX Chlamydia pneumoniae.

XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..928
FT /note= "Mature protein"

FN WO200202606-A2.

PD 10-JAN-2002.

XX 03-JUL-2001; 2001WO-IB01445.

XX 03-JUL-2000; 2000GB-0016363.
PR 11-JUL-2000; 2000GB-0017047.
PR 21-JUL-2000; 2000GB-0017983.
PR 07-AUG-2000; 2000GB-0019368.
PR 18-AUG-2000; 2000GB-0020440.
PR 14-SEP-2000; 2000GB-0022583.
PR 10-NOV-2000; 2000GB-0027549.
PR 22-DEC-2000; 2000GB-0031706.

XX (CHIR-) CHIRON SPA.

XX Ratti G, Grandi G;

XX WPI; 2002-154726/20.

DR N-PSDB; ABL91200.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes

XX Claim 1; Page 57; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding

CC then. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.

XX Sequence 928 AA;

Query Match 41.5%; Score 1982; DB 23; Length 928;

Best Local Similarity 45.2%; Pred. No. 1.9e-121;

Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;

Qy 1 MKSSPPKVFVSTFAIPPLSM-----IATETVLDSSASPDGKNGKNGFVSRESQEDA-GTT 53

Db 1 MKSSLHWFLISSSLALPLSLNFSFAFAAVVEINLGPNTSPSG--PGTYTPPAQTNNADGTI 58

Qy 54 YLPKGNVLENIPTGCTAITKSCENNTKGLDFTGNGNSLLFTQVDVAGVAAVNSSVV 113

Db 59 YNLTDGVSIITN-AGSPALTATSCFETTNLGSFQGHGYQFLQNDIAG--ANCTFNTAA 115

Qy 114 DKSTTFEIGFSSLSFIASPGSSITTKGAVSCSTGSLSTKNVSLFSKFNSTDNGGAI 173

Db 116 NKLLSFGSYLSLIQT--TNATTGTGAIK-STGACSIQSNYSYCFQNFSDNGGALQG 172

Qy 174 KTLUSLGTMTSALFSENSTSKGGAITQSDALTITGNGEVSPDNTSSDGAITEAS 233

Db 173 SSISLS-LNPNLTFAKNKATOKGALYSTGGITINNTLSASFSSENTAANGGAIYTES 231

Qy 234 VTISNNKAVSFIDNKVYTGASSSTTGDMSGGAI CAYKTTSTDTKV-TLTGNQLLFSNNTST 292

Db 232 SFISSNKAISFINNSVTATSA-----TGGAIYCSSTSPKPVLTISDNGELNFINGTAI 285

Qy 293 TAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNT 352

Db 286 TSGGAIYTDNLVLSSGGPTLFKNNSAIDTAAPLGGAI AIDSGLSLSLALGGDITTEGNT 345

Qy 353 V---TSTTPGTNRSSIDLG-TSAKMTALRSAAGRAIFYDPITTTGSSSTTVTVLKNETP 408

Db 346 VVRGASSSTQTTTRNSINIGNTNAKIVQLRASQGNITIFYDPITTTSTAALSDALNLNGPD 405

Qy 409 ADSALQVTGNIIFTGKELSETEADSKNLTSKLLQPVTLTSGGTLTSLKHGVTLOTQFTQQ 468

Db 406 LAGNPAYQGTIVFSGEKLSEAEAEADNLKSTTQQPTTLAGGQLSLKSGVTLVAKSFQS 465

Qy 469 ADSRLEMDVGTTLPEADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTTLLDPT 528

Db 466 PGSTLLMDAGTTLTETADGITINNVLNVDSLSLTKETKATLQATQASQVTLSSLSLVDPS 525

Qy 529 GTFYENHSLRNPQSYDILELKAS--GTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGA 586

Db 526 GNVYEDVSWNNPQVFSCLTTLTADDPANIHIITLADPFLKXNPIMHWGQGNWA--LSWOEDT 584

Qy 587 ST---TATENWTKGYIPNPERIGSLVPSNLSLWNAFIDISSLHLYMETANEGLCQDRAFWC 643

Db 585 ATKSKAATLWTGTYNPNPERRGTILVANILWGSFVDRSIQQLVAIKVRSQSETRGICW 644

Qy 644 AGLSNFFHKDSTKTRGRFRLHSLGGYVIGGNLHTCSDKILSAAPCOLFGRDRDYFAVKNQG 703

Db 645 EGISNFFHKDSTKINKGFRHISAGYVVGATTTLASDNLITAAFCQLFGKORDHFINKRA 704

Qy 704 TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLSGNLSYTHTDNDLTKYTT 760

Db 705 SAYAASLHLQHLATLSS-----PSLLRYLPSSESEQPVLPFAQISYIYKNTMYTYTQ 758

AA99842 standard; Protein: 936 AA.
AA99842;
15-SEP-2000 (first entry)
Chlamydia pneumoniae 98 kDa outer membrane protein CPN100640.
Chlamydia, 98 kDa outer membrane protein; antigen; immunogen; infection;
vaccine; antibacterial; community acquired pneumonia; bronchitis;
sinusitis; acute respiratory disease; upper respiratory tract disease;
asthma; atherosclerosis.
Chlamydia pneumoniae.
Key Location/Qualifiers
Peptide 1..11
/label= Signal_peptide
Protein 12..936
/label= 98_kDa_membrane_protein
WO200032784-A1.
08-JUN-2000.
01-DEC-1999; 99WO-CA01148.
01-DEC-1998; 98US-0110439.
03-MAY-1999; 99US-0132272.
(CONN-) CONNAUGHT LAB LTD.
Murdin AD, Oomen RP, Wang J, Dunn P;
WPI; 2000-412330/35.
N-PSDB; AAA48838, AAA48839.
New polynucleotide encoding the Chlamydia 98 kilobalton outer membrane
protein, useful for preventing or treating Chlamydia infection -
Claim 16; Fig 1; 98pp; English.
The present sequence is CPN100640, the 98 kDa outer membrane protein
from Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of
community acquired pneumonia and upper respiratory tract symptoms and
diseases, including bronchitis and sinusitis. It also has an association
with atherosclerosis and asthma. The 98 kDa outer membrane protein is a
C. pneumoniae-specific antigen which can confer immune protection against
Chlamydia infection. The nucleotide sequence encoding the protein or the
protein itself may be administered as a vaccine to prevent or treat
infection and they may also be used to diagnose infection. The gene
encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA
by PCR.

Search completed: December 16, 2003, 10:52:34
Job time : 50 secs

DB 180 LLSGTSQFASFRNQAFKQGGVYATGTITIIENSPGIVSFQNLAKSGGALSTDMC 239
QY 235 TISNNAKVSFIDNKVTGASSTTGDMSGGAI CAYKTSITDTKVLTCNQMLFNNSTTFA 294
DB 240 SITDNFQVIFDCNSAWEAAQA-----QCGAICC--TTTDTKTLTGKKNLSFTNTALT 292
QY 295 GGAIVYKULEASGGTLTLPNSVNGGTAPK--GGAIAIEDSGELSDSGDIVPLGNT 352
DB 293 GGAISGLKVSISAGGPTLFQSN-IGSSAGQGGGAINIASAGELALSATSGDITFNNQ 351
QY 353 VTSPTGTRSSITDLGTSAKMTALRSAGRAIYFYDPTTGGSTTVDLVKNETPADSA 412
DB 352 VTNGSTST-RNAINIIDTAKVTSIRATQCSYFYDPTINPGTAASDTDLNLNLDANSE 410
QY 413 LQVTGNIIFTGKLSATEAADSKNLTKLQPVTLGGTSLSKHGVTLTQTQAFQADSR 472
DB 411 IEYGAIVFSGEKLSPTEKAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGR 470
QY 473 LEMDVOTTLBPADTS--TINLVINISSIDGAKAKIETKATSKNLTSLGTTLLDPTGTF 531
DB 471 ILMDGGTTLTSAKEANLSLGLAVNLSSLDGTNKAALKTEAADKNLSLGTIALIDTEGTF 530
QY 532 YENHSLRNQSYDILELK--ASGTVTSTAVTDPIMGEKPHYGYOQTGWPVWGTGAST 588
DB 531 YENHLSKASTYPLELLETTAGANGTTILGALSTLTQEPETHYGYQGNW-QLSWANATSS 589
QY 589 -TATFNWTKTYIPNPERIGSLVPSNLWNAFIDISLHYLMETANEGLOQDRAFWAGLS 647
DB 590 KIGSINWTRTYIPSPERKSNLPLNSLWGNFIDIRSIINQLIETKSSGEPERELMLSGIA 649
QY 648 NPFHKDSTKTRRGFRHLSCGYVIGGNLHTCSDKILSNAFCOLFRDRDYFVAKNQGVY 707
DB 650 NFFYRDSMPTRHGFRHISGAYALGTTATTPAEDQLTFAPCOLFARDNRNHTGKNHGT 709
QY 708 GTLYYQHNETYISLPCKL-----RPCSLSVWTEIPVLPFSGNLSYTHTDNDLTKYTTY 761
DB 710 ASLYFPHTEGLFDIANFLWKGKATAPWLSEISQIPLSFDKAFSYLHTDNHMKTYTDN 769
QY 762 PTYKSGWGNDSFALFQGRAPICLDBSALFEQWMPFKLOPVYAHQEGFKEQGTAREBG 821
DB 770 SIKSGWRNDAFCADLGLASLPFVISVPYLKEVEFPVKQVYIYAHQODFYERHAEGRFN 829
QY 822 SSRILVNLALPIGTRFDKESDCQDATYNTLTGYTVDLVRSNPDCTTLRIISGDSWKTGTN 881
DB 830 KSELINVEIPIGVTTFERDSKSEKGYDGLTILMYLDAYRNPCKOTSLIADANMAYGTN 889
QY 882 LARQALVLRAGNHFCFNSNFEAFSQPSFELRGSSRNYNVDLGAQYF 928
DB 890 LARQGSVRAANHFQVNPHEIFCQFAFEVRSRNNYNLGSKFCF 936

Sequence 936 AA;
Query Match 41.2%; Score 1965; DB 21; Length 936;
Best Local Similarity 43.4%; Pred. No. 2.5e-120;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
QY 1 MKSSFPKFFVSTFAIF-PLSMIATETVLDS--ASFDGNKNGNFSVRESOE-DAGTYYLFK 57
DB 1 MKSSVSWLFFSIPPLFSSLSIVAAEVLDSNNSYDGSNGTTFVFTDAAAGTYSLL 60
QY 58 GNVTLLENIPGTGATKSCFNNTKGDLTFTGNGNLLFTQVDAGTVAGAVNSVVDKST 117
DB 61 SDVSFQNALGTLPLASGCGFLFAGGDLTFQGNQHALKFAFINAGSAGTVASTSAADK 120
QY 118 TFIGSSLSFIASPGSSIT-TGKGVSCSTGSLSLTKNVSLFLSKNFSTDNGAITAKTL 176
DB 121 LFNDFSRSLIISCPILLSPTGCALK-SVGNLSLFGNSQIIIFTQNFSSDNGGVINTKNF 179
QY 177 SLTGTMTSALFSENT--SSKKGAIQTSDALITITGNQGEVFSFSDNTSDSGAAIFTEASV 234

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2802.5	58.7	597	4	US-09-198-452A-29	Sequence 29, Appl
2	1940	40.5	930	4	US-09-198-452A-470	Sequence 470, App
3	1917.5	40.2	927	4	US-09-198-452A-472	Sequence 472, App
4	1856	38.9	949	4	US-09-198-452A-478	Sequence 478, App
5	1572.5	32.9	643	4	US-09-198-452A-474	Sequence 474, App
6	1417.5	29.7	922	4	US-09-198-452A-15	Sequence 15, Appl
7	1259	26.4	671	4	US-09-198-452A-468	Sequence 468, App
8	1214	25.4	230	4	US-09-198-452A-30	Sequence 30, Appl
9	1203.5	25.2	507	4	US-09-198-452A-32	Sequence 32, Appl
10	1130	23.7	1132	4	US-09-198-452A-466	Sequence 466, App
11	1126.5	23.6	1006	4	US-09-556-877-190	Sequence 190, App
12	1126.5	23.6	1006	4	US-09-620-412C-190	Sequence 190, App
13	1126.5	23.6	1006	4	US-09-598-419-190	Sequence 190, App
14	1124.5	23.6	982	4	US-09-556-877-176	Sequence 176, App
15	1124.5	23.6	982	4	US-09-620-412C-176	Sequence 176, App
16	1124.5	23.6	982	4	US-09-598-419-176	Sequence 176, App
17	1015.5	21.3	450	4	US-09-198-452A-35	Sequence 35, Appl
18	888	18.6	530	4	US-09-198-452A-482	Sequence 482, App
19	865	18.1	880	4	US-09-556-877-175	Sequence 175, App
20	865	18.1	880	4	US-09-620-412C-175	Sequence 175, App
21	865	18.1	880	4	US-09-598-419-175	Sequence 175, App
22	856	17.9	866	4	US-09-556-877-189	Sequence 189, App
23	856	17.9	866	4	US-09-620-412C-189	Sequence 189, App
24	856	17.9	866	4	US-09-598-419-189	Sequence 189, App
25	834.5	17.5	483	4	US-09-198-452A-27	Sequence 27, Appl
26	821	17.2	494	4	US-09-198-452A-33	Sequence 33, Appl
27	792	16.6	427	4	US-09-198-452A-31	Sequence 31, Appl

QY 569 PHYGYOCTWGPVWGTGASTATFNWTKTGYINPERIGSLVNSLWNAFIDISSLHLYM 628
 Db 421 PHYGYOCTWGPVWGTGASTATFNWTKTGYINPERIGSLVNSLWNAFIDISSLHLYM 480
 QY 629 ETANEGLOGDRAFWAGLGNFPHKDSKTRRGFRHLGGVYVIGNLTCSDKILSAFQ 688
 Db 481 ETANEGLOGDRAFWAGLGNFPHKDSKTRRGFRHLGGVYVIGNLTCSDKILSAFQ 540
 QY 689 LFGDRDYFVAKNGQ-TVYGGTLYYQHNETHYIS-----LPCKLR-PCSLSYYP 734
 Db 541 LFGDRDYFVAKNGQYSLRRNSLLPAQRNLYLSLQTTALFVVLCSYRDSCLFRKP 597

RESULT 2
 US-09-198-452A-470
 ; Sequence 470, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 470
 ; LENGTH: 930
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-470

Query Match 40.6%; Score 1940; DB 4; Length 930;
 Best Local Similarity 43.7%; Pred. No. 5e-139;
 Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;

QY 1 MKSSFPKVFSTPAIFPLSM-IAT---ETVLDSSASFDGKNGNFSVRESQEDAGTYL 56
 Db 1 MKIPLHLLISTLVTILLIATYAGDASISPTDSFDGAGGSTFTPKSTADANGTYVL 60

QY 57 KGNVTLENI PGGTATKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSVVDKS 116
 Db 61 SGNVYI-NDAGKGLTCCCTETETGDLTFTGKGYSFNFVTDAGSNAGAAA-STADKA 118

QY 117 TTFGFSLSPIASPGSITTKGAVSCSTGSLTKNVLNFKNFTSD---NGGAITA 173
 Db 119 LTFTGFSLSPIAAGPTTVASGKSTLS-SAGALNTDNGTILFSONVSEANNNGGAITA 177

QY 174 KTLSTGTMTSALFSENTSSKKGAIQTSALTITGNGEVSFSDNTSSDSGGAIFTEAS 233
 Db 178 KTLISGNTSITITTSNAGKLGAIYSSAAASISGNTGQLVFNNGETGGGALGFEAS 237

QY 234 VTISNAKVFDNKVTGASSSTTGDMSGGGAICAYKTSPTKVTLTQNMQLFSNNTST 293
 Db 238 SSITQNSLFFSGNTATDAAG-----KGGAIYCEKGTETPTLTISGKSLTFAENSST 291

QY 294 AGGAIYVKLEIASGLTLFERNVNGTAPKGAIAIEDSGELSDSGDIVFLGNTV 353
 Db 292 QGGALCAHGLDLSAAGPTLTFNNRCGNTAAGKGAIAIADSGSLSANOGDITFLGNTL 351

QY 354 TSTT-PGTVNRSSIDLTGSAKVTALRSAGRAIYFYDPI---TTGSSTTVTDVLKNVTPA 409
 Db 352 TSTSAPTSTRAIYLGSAKITNLRAAQOGSIYFYDPIASNTTQAS---DVLTIQPD 407

QY 410 DSALYQTNIIPTGKLSLSETAASKNLTSKLPVLSGGLTKLKHGVTLQTAQQA 469
 Db 408 NSPLDYSGTIVFSGEKLGADEAKADNFTSLKQPLALASGTLAKGNVELDVNGPTQTE 467

QY 470 DSRLEMDVGTILEPADTSTIN--NLVINISIDGAKKAKIETKATSKNLTLSGTTILLDP 527
 Db 468 GSTLLMQPGTKLK-ADTEAISLTKLVDLSALEGNSVSIETAGANKTITLTSPLVFQDS 526

QY 528 TGTTFVENHSLRNPOSYDILELKAS-----GTVTSTAVTDPDIPNGERFHYGQGTWG 578
 Db 527 SGNVESHTINCAQTQPLVVFATAAASDIYIDALLTSPVQTPEP-----HYGYQHW 580

QY 579 PIVWGTGASTATFNWTKTGYINPERIGSLVNSLWNAFIDISSLHLYMETANEGLOGD 638
 Db 581 ATWADTSTAKSGTWTWTTGYNPNPERRASVVPDSLWASFTDRTLQQIMTSQANSIQ 640

QY 639 RAFWAGLGNFPHKDSKTRRGFRHLGGVYVIGNLTCSDKILSAFQCFGRDRDYFV 698
 Db 641 RGLWASGTANFPHKDSKTRRGFRHLGGVYVIGNLTCSDKILSAFQCFGRDRDYFV 700

QY 699 AKNGQTVYGGTLYYQHNETHYISLPCKLKRPC--SLSYVPTPIPVLFESGNLSYTTDNDLKT 756
 Db 701 VENTSHNYLASLYLQHRALGGLP--MPSFGSITDMLKDIPLILNAQLSYSTKNDMDT 757

QY 757 KYTYPTVKSGWNSDPALEFGGRAPICL-DESALFQYMPFMKLPVYAHQBFKEQGT 815
 Db 758 RYTSYPEAOGSWTNNSGALELGGSLALYLPKEAPFFQGYFFFLKQFQAVYRQONFKESGA 817

QY 816 EARFEGSSRLVNLALPIGIRPDKESDQDATYNLTGLTVDLVRSNPDCTTLIRISGDSW 875
 Db 818 EARAFDDGDVNCISIPVGIRLEKISEDEKKNFEISLAYIGDVYKKNRSTSLMVSGASW 877

QY 876 KTFGNTLAROALVLRAGNHCFNSNFASFQSFPELGRSSRNYNVDLGAKYQF 928
 Db 878 TSLCKNLARQAFLASAGSHLTLSPHVELSGEAAVELRGSAAHYNVDCGLYSF 930

RESULT 3
 US-09-198-452A-472
 ; Sequence 472, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 472
 ; LENGTH: 927
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; NAME/KEY: SITE
 ; LOCATION: 1...927
 ; OTHER INFORMATION: Xaa=unknown or other
 US-09-198-452A-472

Query Match 40.2%; Score 1917.5; DB 4; Length 927;
 Best Local Similarity 44.8%; Pred. No. 2.6e-137;
 Matches 427; Conservative 147; Mismatches 328; Indels 51; Gaps 22;

QY 1 MKSSFPKVFSTPAIFPLSM-----IATETVLDSSASFDGKNGNFSVRESQEDA-GTT 53
 Db 1 MKSSLHWFLLISSLSLALPLSLNFSAPAFAVVEINLGPNTSFG--PCYTPPAQTNAQGTI 58

QY 54 YLFKGNVTLENI PGGTATKSCFNNTKGDLTFTGNGNSLLFQTVDAGTVAGAAVNSV 113
 Db 59 YNLTGDVSI TN-AGSPALTATACFPKETTGNLSFGHGQYQFLQNI DAG--ANCTFTWTA 115

QY 114 DKSTTFIGFESSLFTASPGSSITTKGAVSCSTGSLTKNVLNFKNFTSDNGGAITA 173
 Db 116 NKLLSFGSFSYLSLQ-T-TNATGTGAIK-STGACSIQSNYSYFCQNFNDNGGALQG 172

QY 174 KTLSTGTMTSALFSENTSSKKGAIQTSALTITGNGEVSFSDNTSSDSGGAIFTEAS 233
 Db 173 SSISLS-LNPULTFAKNKATQKGLYSTGTTINTLNSASFSENTAANGGAIYFAS 231

QY 234 VTISNAKVFDNKVTGASSSTTGDMSGGGAICAYKTSPTKVTLTGQNMQLFSNNTST 292

		Matches		405; Conservative	171; Mismatches	331; Indels	42; Gaps	20;
Qy	1	MKSSPKFVFSTPAIRP--LSMIATETVLDDSGASPDGN-KNGNFSVRESQEDAGTITYLEK	57					
Db	22	MKTSIPFWLVSSVLASCHLOSANEELSPDPSFNGNIDSGTFTPKTS----ATYSLT	77					
Qy	58	GNVTLNIPGTGTAITKSCFNNTKGLTFTGNGNSLLPQTVDAGTVAGAIVNSVVDKST	117					
Db	78	GDVFFYE-PKGKGPLSDSCFKQTTDLNLTFLNGHSLTFFGDFIDAGTHAGAAA-STTANKNL	135					
Qy	118	TFGFSLSFIAPGSGSIITGKAVCSCTGSLSLTKNVSLLSFKNSFTDNGGAIKATKLS	177					
Db	136	TFSGFLLSSDSSFTVTTVTTGQTLG--SAGGVNLENIRKLWAGNFSTADGGAIKGASFL	194					
Qy	178	LTGTTMSALPSENTSSKKGAIOISDALITITGQGVFSFDNTSSDSGAAIFTEASVTIS	237					
Db	195	LTGTSGDALFSNNSSSTKGGAIAITAGARIANNVTGAVFLSNTASTSGGAIDEGTSL	254					
Qy	238	NNAKVSPIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLSFNNSTTTAGGA	297					
Db	255	NNKFLYP-----EGNAAKTT---GGAICTKASGSPELIISNNKTLIFASNVAETSGGA	305					
Qy	298	IYVKLELAEGLTLFERNVNGTAPKGAIAIEDSGELSLSDSGDIIVFLGNVTST--	356					
Db	306	IHAKKLALSGGFTFLRNVSAT-PKGAIAISDASGELSLSAETGNITFVNTLTG	364					
Qy	357	-TPGTNRSDDLGTSAKWTALRSAGRAIYFYPDITTTGSSSTTVDVLKVNTEPADSALQY	415					
Db	365	STDPKRNAINIGSKFTFLRAKNHTIIFYDPIT--SEGTSSDVLKINNGSAGALNPY	422					
Qy	416	TGNIIFTGEKLSATEAADSKNLTSKLPQVTLSSGTLSLKHGVTLOQATFQOADSLEM	475					
Db	423	QGTILFSETLTADLVADNLKSSFTQPVSLSGKLLQKGVLTLESTSPSQEAGSLGM	482					
Qy	476	DVGTTLB-PARTSTINNLVINISSIDGAKAKIETKATSKNLTLISGTLILDDPTGTYYEN	534					
Db	483	DSGTTLTSTAGSIITNLGINVDSLGLKQPVSLTAKGASNKVIYSGKLNLDIDEGNIYES	542					
Qy	535	HSLRNPQSYDILELKASGTVTS---TAVTPDPIMGEKPHFYGYGTGPIVWGTGASTT-	589					
Db	543	HMFSDQLFSLKLTVDADVDTNVDISLIPVPAEDPNSSEYFGQGNW-VNWTDTATNT	601					
Qy	590	--ATFNWTKTGYIPNPERIGSLVPSNLWNAFIDISLHLYMETANEGLQGDRAFWCAGLS	647					
Db	602	KEATATWTKTGFVSPERKSALVNTLWGVTDTRSLQQLVEIGATGMEHKQGFVWSMT	661					
Qy	648	NFFHKDSTKTRGFRHLGGVIGGNLHTCSDKILSAAPCOLFORDRDYFVAKNQGTYYG	707					
Db	662	NFLHKTGDNKGRHTSGGVYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIHNNSTYTG	721					
Qy	708	GTLYYQHNET-----YISL-PCKLRPCSLSYVPTETPVLFSGNLSYTHTDNDLTKYTTY	761					
Db	722	GTLPFKHSHTLQPNYLRLGRAKFSESAIEKFPREIPALDVQVFSFSDHDMETHYTSL	781					
Qy	762	PVTKSGWNGDSFALFEGGRAPICLI--DEGALFEQYMPFMKLOFVYAHQGFKEQGTAREF	820					
Db	782	PSBSGSWNECIAGIGLDLPVLSNPHLPKFTFIPQMKVEMVYVSQNSFFSESSDGRGF	841					
Qy	821	GSSRLVNLALPIGIRFDKESDQDA-TYNLTLYGTVDLVRNPDCTTTTLRISGGSWKTFG	879					
Db	842	SIGRLNLNLSIPVGAKF-VQGDIGDSYTYDLSGFFVSDVVRNPNQSTATLVMSPDWSKIRG	900					
Qy	880	TNLARQALVLRAGNHFCNFSNFEAFSQFSFELRGSSRNYYNDLGAKYQF	928					
Db	901	GNLSRQAFLLRGSSNNYVYNSNCELFHYAMELRGSSRNYYNDVGTGLRF	949					
RESULT 5								
US-09-198-452A-474								
; Sequence 474, Application US/09198452A								
; Patent No. 6559294								
; GENERAL INFORMATION:								
; APPLICANT: Griffais, R.								
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments								
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention								
; TITLE OF INVENTION: and treatment of infection								
; FILE REFERENCE: 9710-003-999								
; CURRENT APPLICATION NUMBER: US/09/198,452A								
; CURRENT FILING DATE: 1998-11-24								
; NUMBER OF SEQ ID NOS: 6849								
; SEQ ID NO 478								
; LENGTH: 949								
; TYPE: PRT								
; ORGANISM: Chlamydia pneumoniae								
; FEATURE:								
; NAME/KEY: SITE								
; LOCATION: 1...949								
; OTHER INFORMATION: Xaa=unknown or other								
US-09-198-452A-478								
Query Match								
38.9%; Score 1856; DB 4; Length 949;								
Best Local Similarity								
42.7%; Pred. No. 1.3e-132;								

RESULT 5
US-09-198-452A-474
; Sequence 474, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.

Wed Dec 17 09:17:09 2003

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 474
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-474

Query Match 32.9%; Score 1572.5; DB 4; Length 643;
Best Local Similarity 49.8%; Pred. No. 2.6e-111;
Matches 314; Conservative 93; Mismatches 209; Indels 15; Gaps 6;

QY 308 GGTLFSSRVNGGTPAPKGAIAIEDSGELSLSDSDIVFLGNTVTSTTP-GTNRSSID 366
D 18 GGGISFNNIVQTTAGNGGALISLAAGCSLSAEAGDITFNGNAIVATTPQTKRNSID 77
QY 367 LGTSAXMTALRSAGRAIFYDPITTTGSSSTTVVDLKNVETPADSALQYTGNIIFTGKEL 426
D 78 IGSTAKITNLRALSCHSIFPYDITANTADSTDLNKNKADAGNSTDYSGSIVFSGKEL 137
QY 427 SETEAADSKNLTKLLOPVTLGGTISLKHGVTLOTAFTQQQADSLMDVGTITLEPA-D 485
D 138 SEDEAKVADNLSTLQPVTLTGNLVLKRGVLTDKGTQTAGSSVIMDAGTTLKASTE 197
QY 486 TSTINNLVINISSIDGAKKAIETKATSKNLTSGLTILDDPTGFVENHSLRNPQSYDI 545
D 198 EVTLTGLSIPVDSLGBGKVVVIAASAKRNVALSGPILLDDNQNAYENDHDKTQDFSP 257
QY 546 LELKASGTVTSTAVTPDIPIMGEKPHYGYQGTWGPVW-----GTGASTTATFNWTKGYI 600
D 258 VQSLAGTATTDVPAVPTVATPHYGYQGTW-G-MTWVDDTASTPKTKTATLAWTNTGYL 316
QY 601 PNPERRIGSLVPSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNPFHKDSTKTRG 660
D 317 PNPERRQGLVPSLWGSFSDIQAIOGVIERALSALTLCSDRGFWAAGVANFLDKCKGKRX 376
QY 661 FRHLSGGVYVGNLHTCSDKLSAFCOLGRDREYFVAKNQCVYGGTYLYQHNEYIS 720
D 377 YRHSGGYALGGAAQTCSENLSIFAFQGLFSDKDFLVAKNHTDTYAGAFYIQL-----IT 432
QY 721 LPCKLRPCSLSYVP---TEIPVLPFGSLSYTHTDNLTKYTTYPTVKGSGWGNDSFALEF 777
D 433 ECSCFICGLLDKLPGSWSHKLVLLEGQALYSHVSNLTKYTAYPEVKSGWGNNAFNML 492
QY 778 GGRAPICLDESALPEQYMPFMKLOFVYAHQBGFEQGTAEAREFGSSRLVNLALBPIGRFD 837
D 493 GASSHSYPEYLHCFDTPAYIKLNLTYIRODSFSEKGTGEGRSFDDSNLNLSLPIGVKFE 552
QY 838 KESDCODATYNLTGYTVDLVRSNPDCTTLRISGDSWKTFTGLARQALVLRAGNHFCF 897
D 553 KFSPCNDYSYDLSYVDLIRNDPKCTTALVISGASWETVANNLARQALQVRAGSHYAF 612
QY 898 NSNPEAFQGFELRGSSRNYNVDLGAKYQF 928
D 613 SPMEVLQGFVEVRGSSRIYNVDLGKQFQF 643

RESULT 6
US-09-198-452A-15
; Sequence 15, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 15
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...922
; OTHER INFORMATION: Xaa=unknown or other
; US-09-198-452A-15

Query Match 29.7%; Score 1417.5; DB 4; Length 922;
Best Local Similarity 36.5%; Pred. No. 2.9e-99;
Matches 347; Conservative 156; Mismatches 385; Indels 63; Gaps 26;

QY 5 PP-KPVFTFAIFPLSMIATETVLDSSASFDGNKNGFVSRESQEDAGTTLFKGNVTLE 63
D 8 PFLVFSFTLLSVFDTLSLATTISLTPEDSFHGDSQN--AERSYNVQAGDVVSLTGDVSL 65
QY 64 NIPGTGTAITKCPNNTKGDLTFTGNGNSLLFTQVDAGTVAGAAVSSVVDKSTT-FIGF 122
D 66 NV--DNSALNKACFVTSVTSFAGHHGXYPNNISSGTTKEGAVLCCODPQATARFSGF 123
QY 123 SLSLFTASPGSSITTKGAVSC--STGSLSTKFNVSLLSFKNFTDNGGAIKATLSLTG 180
D 124 STLSPNQSPGDIKEQ-----CLYSKNALMLLNYYVVRPEQKQSKTKGGAISGANVTIVG 178
QY 181 TTMSALFSENSTSKKGGAIOQTSDALTIITGNQGEVSFSDNTSSD-SCAAIFTASVTISNN 239
D 179 NYDSVSFYQNAAT-FGGAIHSSGPIQIAVNOABIRFAQNTAKNGSGGALYSGDDIDON 237
QY 240 AKVSFIDNKTVCASSSTTGDMSGCAICAYKTSTDTK---VTLTGNQMLLFSNNTSTTAG 295
D 238 AVLVFRENE-----AUTTAIGKGAVCCLPITSGSSTPVPVITFSDNKQLVFRNHIMG 292
QY 296 GAIYVKKLELASGLTLFERNVNGTAPKGAIAIEDSGELSLSDSDGDIIVFLGNTVTS 355
D 293 GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGEISLSAEKGTITFQGN--RT 350
QY 356 TPTGTNRSSIDLTSAXMTALRSAGRAIFYDPITTTGSSSTTVVDLKNVETPADSALQY 415
D 351 SLSPFLN--GIHLNQNAKFLKLQARNGYSIFDYDPII--SEADGSTQLNINGDPKKN--EY 404
QY 416 TGNIIPTGKELSTEADSKNLTKLLOPVTLGGTISLKHGVTLOTAFTQQADSRLEM 475
D 405 TGIILFSGEK--SLANDPRDPKSTIPQNVNLASGLVIVKEGAETVSKTQSPGSHLV 461
QY 476 DVGTTL-EPADTSTINNLVINISSIDGAKKAK-IETKATSKNLTLSTGTTILLDPTGTFYE 533
D 462 DLGKTLFASKEDIAITGLAIDIDSLSSSTAATAVIKANTANKQISVTDSEIISPTGNAYE 521
QY 534 NLSLRNPQSDVILELK--ASGTVTSTA-----VTPDPIMGEKPHYGYQGTWGPVW-GTG 585
D 522 DLRRNSQTPTLLSLEFGAGGSVTVTAGDFLPVSP-----HYGFGQNW-KLAWTGTG 572
QY 586 ASATTATNTWTKGYIPNPERIGSLVPSLWNAFIDISSLHYLMETANEGLQGDRAFWCAG 645
D 573 -NKVGEEFWDKINKYPRPEKEGNLVFNILWGNADVRSALMQVQETHASSLQTDRLWIDG 631
QY 646 LSNFFHKDSTKTRRGFRHLGGYVIGNHLHTCSDKLSAFCQLFGDRDRDYFVAKNQGTV 705
D 632 IGNLFHVSASEDNIRYRHNSGGYVLSVNNETTPKHYSMAFSQSLFSRDKDYAVSNNEYRM 691
QY 706 YGGTYLYQHNET-----YISLPCKLRPCSLSYVPTPIP-VLFSGNLSYTHTDNLTKY 758
D 692 YLGSYLYQYTTSLGNIIFRYASRNPNVNVGLISRRFLQNLPMIFHLCAIGHATNMKTDY 751
QY 759 TTYPTVKGSGWGNDSFALEFGGRAPICLDESA-LFEQYMPFMKLOFVYAHQBGFEQGTGTEA 817
D 752 ANFPVWKNWRNWCWALIECGGSMELLVFENGRILFQGAIPFMKLOLVYAYQGFKEATTAG 811
QY 818 REFSSRLVNLALPIGIRFDKESQCDATYNLTGYTVDLVRSNPDCTTLIRISGDSWKT 877

Db 590 KIGSINWTRITGYIPSPERKSNLPLNSLWGNFIDIRSNQLIETKSSGEPFREY 643

RESULT 8

US-09-198-452A-30

; Sequence 30, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 30

; LENGTH: 230

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-30

Query Match 25.4%; Score 1214; DB 4; Length 230;

Best Local Similarity 99.6%; Pred. No. 1e-84;

Matches 226; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 702 QGTVVGTLVYOHNETYISLPCKLRPCSLSYVPTPEIPVLFSGNLSYTHTDNDLTKYTTY 761

Db 4 KGTVVGTLVYOHNETYISLPCKLRPCSLSYVPTPEIPVLFSGNLSYTHTDNDLTKYTTY 63

QY 762 PTVKGSGNDSFALFEGGRAPICLDESALFEQYMPFMKLOFVYAHQEGKEQGTAREFG 821

Db 64 PTVKGSGNDSFALFEGGRAPICLDESALFEQYMPFMKLOFVYAHQEGKEQGTAREFG 123

QY 822 SSSLNVALPIGIRPKESDCQDATYNTLGYTVDLVRSPDCTTLIRSGDSWKTEGNTN 881

Db 124 SSSLNVALPIGIRPKESDCQDATYNTLGYTVDLVRSPDCTTLIRSGDSWKTEGNTN 183

QY 882 LARQALVLRAGNHFCFNSNFEAFSQSFELRGSSRNVDLGAKYQF 928

Db 184 LARQALVLRAGNHFCFNSNFEAFSQSFELRGSSRNVDLGAKYQF 230

RESULT 9

US-09-198-452A-32

; Sequence 32, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 32

; LENGTH: 507

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-32

Query Match 25.2%; Score 1203.5; DB 4; Length 507;

Best Local Similarity 45.9%; Pred. No. 2.2e-83;

Matches 235; Conservative 82; Mismatches 155; Indels 19; Gaps 7;

QY 436 NLTSKLLQPVTLTSGGTLSSKHGVTLOTQAFQQADSRLEMDVGTLE-PADTSTINNLVI 494

Db 18 NLKSTFTQAVELAGALVLDGVTIVVANTITQVSGSKVMVMDGGTTFEASAGVTINGLAI 77

QY 495 MISSIDGAKKAKIETKATSKNLTSGTITLLDPTGTFVENHSLRNPSQSDILELKASCTV 554

Db 78 NIDSIDGTNKAIIRATAASKDVALSGPIMLVDAQNYEHNLSQQQVFAILIELSAQGTM 137

Db 812 RRFNSGSLTSSVPLGIRPEKALQDVLDFSFYIDIPFKDPSCEAALVISGDSMLV 871

QY 878 FGTNLARQALVLRAGNHFCFNSNFEAFSQSFELRGSSRNVDLGAKYQF 928

Db 872 PAHVRSHAFVSGTGRYHFNDDYELLCSIECPHARNYINCSKFRP 922

RESULT 7

US-09-198-452A-468

; Sequence 468, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 468

; LENGTH: 671

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-468

Query Match 26.4%; Score 1259; DB 4; Length 671;

Best Local Similarity 42.8%; Pred. No. 2e-87;

Matches 280; Conservative 130; Mismatches 220; Indels 24; Gaps 15;

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Db 1 MKSSVSUWLFSSIPFLSSLSIVAAEVLDSNNNSYDGSNGTTFVFTSTTDAAGATYSLL 60

QY 58 GNTYLENIPTGTATKSCFNNTKGLTFTGNGNSLLFQTVDAAGTAVAGNSVVDKST 117

Db 61 SDVSFQAGALGIPLAGSCFLEAGDLTFQNHQALAFINAGSSAGTAVASADKNL 120

QY 118 TFIGFSSLSFIASPGSIT-TGKAVSCSTGSLTKNVSLLFSKNFSTNDGGAITAKTL 176

Db 121 LFNDFSLSLIISCPSSLISPTGQALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF 179

QY 177 SLTGTMTSALFSENT--SSKKGGAIOQSDALITITGNGEVSFSDNTSSDGAIFTEASV 234

Db 180 LLSGTSQFASFRNQAFQKGGVYATGTTIENSFGIVSFQNLAKSGGALYSTDNC 239

QY 235 TISNNAKVSFDINKVTGASSSTTGMGGAICAYKTTDTKVTLTGQMLLFSNNTGTA 294

Db 240 SITDNFQVIFDNGSAAEAQA-----QGAICCC--TTIDKVTLTGKNKLSFTNTALT 292

QY 295 GGALVYKLELASGGLTIFRSNVNGGTAPK--GGAIAIEDSGELSLSDSGDIVFLGNT 352

Db 293 GGALISGLKVSISAGGPTLFQSN-ISGSSAGQGGGAINIASAGELALSATSDDITFNNQ 351

QY 353 VTSTTPGNRSIDLGTSKAKTALRSAGRAIYFDPTTSSSTVTDVLKVNTPADSA 412

Db 352 VTNGSTST-RNAINIIDTAKVTSRAATGQSIYFDPTNPGTAASTDTLNLNLANSE 410

QY 413 LOYTGNITFTGEKLSATEAASDKNLSKLLQPVTLTSGGTLSSKHGVTLOTQAFQQADSR 472

Db 411 IEYGAIYFSGEKLSPTEKAIANVTSTIROPVAVLARGDLVRDGVVTFKOLTSQPSR 470

QY 473 LEMDVGTTLEPADTS-TINNVLINSSIDGAKKAKIETKATSKNLTSGTITLLDPTGTF 531

Db 471 ILMDGGTILSAKANLSLAVNLSSLDGTNKAALKATEADKNLSLSSTIALIDTEGTF 530

QY 532 YENHSLRNPSQSDILELK---ASGTVTSTAVTPDPIMGEKPHYGQGTWGPVWGTGAST 588

Db 531 YENHNLKSASTYPLLELTITAGANGTITLGAISLTLLQBPETHYGYQGNW-QLSWANATSS 589

QY 589 -TATFNWTKGTGIPNPERIGSLVFNLSLWNAFTDISLHVLMEANEGLOGDRAF 641

Db 597 DRYDWLGSNQKINVLKQL-GTKPPANAPSDLTGEMPKYGYQGSW-KLAWDPNTANNG 654
QY 591 TP-----NWTKTGYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFWCAGL 646
Db 655 PYTLKATWTKTGYNPGPERVASLVPSNLWGSILDIRSAHSAIQASVDGRSYCRGLWVSGV 714
QY 647 SNFFHXDSTKTRRGRHLSGGYVIGGNLHTCSDKILSAAFCOLFCGRDRDYFVAKNQGTVY 706
Db 715 SNFFYHDDRDLGQGYRYISGGYSLGANSYFGS-SMEGLAFTVEVFGSKDYVVCRSNHHAC 773
QY 707 GGTLYYQHNETYISLPCKLPCSLSYVTEIPVLPFG---NLSYTHDNDLTKYTYTPT 763
Db 774 IGSVYLSQQAL-----CG-SY-----LFGDAFIRASYGFGNQHMKTSYTFABE 816
QY 764 VKGSWGNDSFALEFGGRAPICLDESALP-EQYMPFMKLOFVYAHQEGFKEQGTAEAREFGS 822
Db 817 SDVRWNNCLAGEIGAGLPVITPSKLYLNLRLPFVQAEFSYADHESFTEEGDQARAFKS 876
QY 823 SRLVNLALFIRPDKESQDQATYNLTGVTVDLVRSNPDCTTTLRISGDSWKTFTGNL 882
Db 877 GHLLNLSPVGVKFDRCSTHPNKYSFMAAYICDAYRTISGTETTLSSHQETWTTDAFHL 936
QY 883 ARQALVLRAGNHCNFSNFEAFSQFSFELRGSSRNYNVDLGAKYOF 928
Db 937 ARHGVVRGSMYASLTSNIEVYGHGREYEDASRGYGLSAGSKVXP 982

Search completed: December 16, 2003, 10:55:18
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2003, 10:54:06 ; Search time 37 Seconds

(without alignments)
4664.671 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFPKVFSTFAIFPLSM.....FELRGSSRNYNVDLGAQYQF 928

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4774	100.0	928	12	US-09-428-122-2
2	1965	41.2	936	9	US-09-452-380-3
3	1965	41.2	936	12	US-10-324-129-3
4	1946.5	40.8	925	9	US-09-452-380-4
5	1946.5	40.8	925	12	US-10-324-129-4
6	1915	40.1	926	12	US-09-738-269-57
7	1915	40.1	926	14	US-10-023-437-57
8	1656.5	34.7	839	12	US-09-738-269-23
9	1656.5	34.7	839	14	US-10-023-437-23
10	1437.5	30.1	922	9	US-09-886-468-19
11	1126.5	23.6	1006	9	US-09-841-132-190
12	1124.5	23.6	982	9	US-09-841-132-176
13	865	18.1	880	9	US-09-841-132-175
14	856	17.9	866	9	US-09-841-132-189
15	851.5	17.8	679	12	US-09-738-269-53

16	851.5	17.8	679	14	US-10-023-437-53	Sequence 53, Appl
17	737.5	15.2	439	9	US-09-841-132-524	Sequence 524, App
18	685.5	14.4	931	10	US-09-779-081-2	Sequence 2, Appli
19	685.5	14.4	1609	12	US-09-841-260-75	Sequence 75, Appl
20	685.5	14.4	1609	14	US-10-007-693-75	Sequence 75, Appl
21	672.5	14.1	978	12	US-09-841-260-65	Sequence 65, Appl
22	672.5	14.1	978	14	US-10-007-693-65	Sequence 65, Appl
23	666	14.0	1723	9	US-09-841-132-394	Sequence 394, App
24	666	14.0	1723	9	US-09-841-132-395	Sequence 395, App
25	608	12.7	871	9	US-09-886-468-21	Sequence 21, Appl
26	597	12.5	1016	12	US-09-841-260-95	Sequence 95, Appl
27	597	12.5	1016	14	US-10-007-693-95	Sequence 95, Appl
28	582	12.2	1530	9	US-09-841-132-178	Sequence 178, App
29	580.5	12.2	963	9	US-09-886-468-22	Sequence 22, Appl
30	576.5	12.1	1531	12	US-09-841-260-98	Sequence 98, Appl
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32	559	11.7	1751	9	US-09-841-132-445	Sequence 445, App
33	559	11.7	1751	9	US-09-841-132-594	Sequence 594, App
34	559	11.7	1752	9	US-09-841-132-180	Sequence 180, App
35	546.5	11.4	964	9	US-09-841-132-177	Sequence 177, App
36	546.5	11.4	977	9	US-09-841-132-191	Sequence 191, App
37	523	11.0	1770	9	US-09-841-132-444	Sequence 444, App
38	513	10.7	1776	9	US-09-841-132-179	Sequence 179, App
39	502	10.5	848	9	US-09-841-132-192	Sequence 192, App
40	490.5	10.3	948	9	US-09-841-132-194	Sequence 194, App
41	477.5	10.0	514	9	US-09-886-468-23	Sequence 23, Appl
42	394	8.3	691	9	US-09-841-132-313	Sequence 313, App
43	385	8.1	162	12	US-09-738-269-55	Sequence 55, Appl
44	385	8.1	162	14	US-10-023-437-55	Sequence 55, Appl
45	344	7.2	700	9	US-09-841-132-345	Sequence 345, App

ALIGNMENTS

RESULT 1

US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-428-122-2

Query Match	100.0%;	Score 4774;	DB 12;	Length 928;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 928;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTTLFPGNV	60	
Db	1	MKSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTTLFPGNV	60	
QY	61	TLENIGTGTATKSCFNNTKGLTFTGNLSLLFOTVDAGTVAGAAVNSVVDKSTTFI	120	
Db	61	TLENIGTGTATKSCFNNTKGLTFTGNLSLLFOTVDAGTVAGAAVNSVVDKSTTFI	120	
QY	121	GFSSLSFIAPSGSIITTKGAVSCSTGSLTKNLSLLFSKNFSTDNGGAITAKTSLTG	180	

Db 121 GFSSLSFIASPGSSITTTGKGVSCSTGSLSTKVNLSLLFKNFSTDNGGAITAKTLTSG 180
 Qy 181 TTMSALFSENTSSKGGGAIQTSALDTITGNQGEVSFSDNTSSDGAALFTEASVTISNNA 240
 Db 181 TTMSALFSENTSSKGGGAIQTSALDTITGNQGEVSFSDNTSSDGAALFTEASVTISNNA 240
 Qy 241 KVSFIDNKVTCASSTTGDMSGGAICAYKTSITDVKTLTGNQMLLFNSNTSTTAGGAIYV 300
 Db 241 KVSFIDNKVTCASSTTGDMSGGAICAYKTSITDVKTLTGNQMLLFNSNTSTTAGGAIYV 300
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 Db 301 KKLLEASGLTLFNRNSVNGTAPKGGAIATEDSGELSLSDSGDIIVFLGNVTSTTTPGT 360
 Qy 361 NRSSIDLGTSAKMTALRAAGRAIYFYDPIITGSSSTTVDLKYNETPADSALQYTCNII 420
 Db 361 NRSSIDLGTSAKMTALRAAGRAIYFYDPIITGSSSTTVDLKYNETPADSALQYTCNII 420
 Qy 421 FTGEKLSFTEAADSNNLSKLLQPVTLISGGTILSLKHGVTLOTQAFQOADSRLMDVGT 480
 Db 421 FTGEKLSFTEAADSNNLSKLLQPVTLISGGTILSLKHGVTLOTQAFQOADSRLMDVGT 480
 Qy 481 LEPADTSIINNVINISIDGAKAKIETKATSKNLTLSGTTITLDPGTGFYENHSLRNP 540
 Db 481 LEPADTSIINNVINISIDGAKAKIETKATSKNLTLSGTTITLDPGTGFYENHSLRNP 540
 Qy 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGASTTATFNWTKTYI 600
 Db 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGASTTATFNWTKTYI 600
 Qy 601 NPPEIGSLVNSLWNAIDISSLHYLMETANEGLQDRAFWCAGLSNFHKSSTKTRRG 660
 Db 601 NPPEIGSLVNSLWNAIDISSLHYLMETANEGLQDRAFWCAGLSNFHKSSTKTRRG 660
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RESULT 2

US-09-452-380-3
 ; Sequence 3, Application US/09452380
 ; Patent No. US20020094340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MURDIN, Andrew D.
 ; APPLICANT: COHEN, Raymond P.
 ; APPLICANT: WANG, Joe
 ; APPLICANT: DUNN, Pamela
 ; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
 ; FILE REFERENCE: 032931/0216
 ; CURRENT APPLICATION NUMBER: US/09/452,380
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: US 60/132,272
 ; PRIOR FILING DATE: 1999-05-03
 ; PRIOR APPLICATION NUMBER: US 60/113,439
 ; PRIOR FILING DATE: 1998-12-01

; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 936
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-452-380-3
 Query Match 41.2%; Score 1965; DB 9; Length 936;
 Best Local Similarity 43.4%; Pred. No. 1.6e-138;
 Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
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 Db 61 SDVSTQNALGIPILASGCFLEAGDGLTFQGNQHALKAFAPINAGSSAGTVASTAAADKL 120
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 Db 180 LUSGTSQAFSFRNOAFTKQGVVYATGTITIENSPIGVFSQNLAKSGGALYSTDNC 239
 Qy 235 TISNNAKVFIQNKVTGASSSTTGDMSGGAICAYKTSITDVKTLTGNQMLLFNSNTSTA 294
 Db 240 SITDNFQVIFDGNSAWEAQA-----QGAICC--TTTDKVTLTGKNLSFTNNALTY 292
 Qy 295 GGAIVYKLEASGLTLFNRNSVNGTAPK--GGAIAIEDSGELSLSDSGDIIVFLGN 352
 Db 293 GGAISGLKVSISAGGPTLFQSN-1SGSAGQGGGAINIASAGELALSATSGDITFN 351
 Qy 353 VSTTPTGWNRSIDLTGSAKMTALRAAGRAIYFYDPIITGSSSTTVTLVKNETPADSA 412
 Db 352 VINGSTST-RNAINIDTAKVISIRAAFGOSIYFDDITNPGTAASTDTLNLNADANSE 410
 Qy 413 LQYTGNIITFGKLSFTEAADSNNLSKLLQPVTLISGGTILSLKHGVTLOTQAFQOADS 472
 Db 411 IEYGAIVPSGKLSFTEKAIAANVTSTIRQAVLARGDLVLRDGVTVTFKDLTQPSGR 470
 Qy 473 LENDVGTTLPEADTS-TINNIVINISIDGAKAKIETKATSKNLTLSGTTITLDPGTGF 531
 Db 471 ILMGDTTILSAKEANLSLGNLAVNLSSLDGTNKAALKTEADKNISLSGTLALIDTGSF 530
 Qy 532 YENHSLRNQSYDILELK---ASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTGAST 588
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 Qy 589 -TATFNWTKTYIPNPERIGSLVPSNLSWNAFIDISLHYLMETANEGLQDRAFWCAGLS 647
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Db 300 FQSN- ISGSSAGQGGGAINIASAGELALSATSATGDTITNNQVINGSTST-RNAINIIDT 357
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Qy 431 AADSKNLTKLQPVTLGGTSLKHGVTLOTQAFQOQADSRLEMDVGTTLLEPADTS-TI 489
Db 418 KAIAANVTSTIROPAVLARGDLVLDGVTVPFKDLTQSPGRILMDGGTTLISAKENL 477
Qy 490 NNLVINISIDGAKAKIETKATSKNLTLSGITILDDPTGTYENHSLRNPOSYDILELK 549
Db 478 NGLAVNLSLDTGNTKAALKEADKNIISLGSITIALIDTEGTFYENHSLKASTYPLEL 537
Qy 550 ---ASGTVTSTAVTDPDPINGEFHYGYQGTWGPVIMVGTGAST-TATFNWTKTYIPN 605
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Qy 606 IGSVLPNSLWNAFIDISSLHYLMETANEGLQDRAFWCAGLSNFFHKDSTKTRRGRHLS 665
Db 597 KSNLPLNSLWGNFIDIRSINQLIETKSGEPFERELMWSGIANFFYRDSMPTRHGRHS 656
Qy 666 GGYVIGGNLHTCSDKILSAFQOLGCRDRDYFAKNQGVYGGTLYYQHNETYISLPCKL 725
Db 657 GGYALGITATTAPEDQLTFAFQOLFARDNRNHTGKNHGDYTGASLYFHHTEGLFIANFL 716
Qy 726 -----RPSLSVVPTEIPVLSGNLSYTHDNDLTKYTYTTPVKSGNDSFALFEGG 779
Db 717 WKGATRAPVWLSEISQIIPLSFPAKFSYLTDNHNMTYTDNSIIKGSWRNDAFCADLGA 776
Qy 780 RAPICLDESALFQYMPFVKQVYAHQGFKEQGTAREFGSSRLVNLALPIGIRFDKE 839
Db 777 SLFPVISVPLLKEVFPVKVQYIAHQODFYERHAEGRAFNKSSELINVEIPIGVTFERD 836
Qy 840 SDCQDATYMLTGYTVDLVRNPDCTTLIRISGDSWKTGTNLARQALVLRAGNHCFNS 899
Db 837 SKSEKGYDITLMIYILDVARNPKQTSLSIASDANWMAIYTNLARQGFVRAANHFQVNP 896
Qy 900 NFEAFQSFPELGRSSRNVDLGAQYF 928
Db 897 HMEIFQFAFEVRSRNNYNTNLGSKPCF 925

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RESULT 5
US-10-324-129-4
; Sequence 4, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-324-129-4

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Query Match 40.8%; Score 1946.5; DB 12; Length 925;
Best Local Similarity 43.5%; Pred. No. 3.8e-137;
Matches 404; Conservative 177; Mismatches 319; Indels 29; Gaps 15;
Qy 18 LSMIATETVLDS-ASPDGKNGNFSVRESOE-DAGTYLFGKNVTLENIPCTGTATKS 75
Db 8 LSIVAAEVTLDSSNNSDGSGNTTFTVSTDDAAAGTYSLLSDVSFQAGALGIPLASG 67

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Qy 76 CFNNTKGLDTFTNGNSLLFQTVDAAGTVAGAAVNSSVVDKSTTTFIGFSSLSFIASPGSSI 135
Db 68 CFLEAGDGLTFQGNHAKLAFINAGSAGTVASTAADKNLLENDFSRSLISICPSLL 127
Qy 136 T-TGKGAIVSCSTGSLSTLKNVLSLFSKFNSTDNGGAIKTAKTSLTGTMTGALFSENT--S 192
Db 128 SPTQCCALK-SVGNLSLTGNSQIIFTFQFSDNGGVINTKNFLSLGTSQSFASFRNQAF 186
Qy 193 SKKGALQTSALITITNGQEVSDNTSSDGAITEASVTISNNAKVSFIDNKVTGA 252
Db 187 GKQGGVYATITTIENSPIGVSPSONLAKSGGALYSTDNCSITDNPQVIFDGNASWEA 246
Qy 253 SSSITGDMSGCAICAYKTSITKVTLCNOMLLFSNNTTGTAGAIYVKKLELASGGLTL 312
Db 247 AQA-----QGAICG--TTTDTKVTILGNKNLSFTNTALTYYGSAISGLKVISAGGPTL 299
Qy 313 FSRNSVNGGTAPK--GGAIAIEDSGELSDSADSGDIVELGNVTSTTPTGTVNRSSIDIGTS 370
Db 300 FQSN- ISGSSAGQGGGAINIASAGELALSATSATGDTITNNQVINGSTST-RNAINIIDT 357
Qy 371 AKMTALRAAGRAIYFDPITGSSITVDLVKNETPADSALQVGTGNIIFTEGKLSETE 430
Db 358 AKVTSIRAATGSIYFYDPITNPGTAASDTINLNLADANSEIEYGGAIYFSGEKLSPTE 417
Qy 431 AADSKNLTKLQPVTLGGTSLKHGVTLOTQAFQOQADSRLEMDVGTTLLEPADTS-TI 489
Db 418 KAIAANVTSTIROPAVLARGDLVLDGVTVPFKDLTQSPGRILMDGGTTLISAKENL 477
Qy 490 NNLVINISIDGAKAKIETKATSKNLTLSGITILDDPTGTYENHSLRNPOSYDILELK 549
Db 478 NGLAVNLSLDTGNTKAALKEADKNIISLGSITIALIDTEGTFYENHSLKASTYPLEL 537
Qy 550 ---ASGTVTSTAVTDPDPINGEFHYGYQGTWGPVIMVGTGAST-TATFNWTKTYIPN 605
Db 538 TAGANGTITLGAISTLTLOQEPETHYGYQGNW-QLSWANATSSKIGSINWTRTGYIPSP 596
Qy 606 IGSVLPNSLWNAFIDISSLHYLMETANEGLQDRAFWCAGLSNFFHKDSTKTRRGRHLS 665
Db 597 KSNLPLNSLWGNFIDIRSINQLIETKSGEPFERELMWSGIANFFYRDSMPTRHGRHS 656
Qy 666 GGYVIGGNLHTCSDKILSAFQOLGCRDRDYFAKNQGVYGGTLYYQHNETYISLPCKL 725
Db 657 GGYALGITATTAPEDQLTFAFQOLFARDNRNHTGKNHGDYTGASLYFHHTEGLFIANFL 716
Qy 726 -----RPSLSVVPTEIPVLSGNLSYTHDNDLTKYTYTTPVKSGNDSFALFEGG 779
Db 717 WKGATRAPVWLSEISQIIPLSFPAKFSYLTDNHNMTYTDNSIIKGSWRNDAFCADLGA 776
Qy 780 RAPICLDESALFQYMPFVKQVYAHQGFKEQGTAREFGSSRLVNLALPIGIRFDKE 839
Db 777 SLFPVISVPLLKEVFPVKVQYIAHQODFYERHAEGRAFNKSSELINVEIPIGVTFERD 836
Qy 840 SDCQDATYMLTGYTVDLVRNPDCTTLIRISGDSWKTGTNLARQALVLRAGNHCFNS 899
Db 837 SKSEKGYDITLMIYILDVARNPKQTSLSIASDANWMAIYTNLARQGFVRAANHFQVNP 896
Qy 900 NFEAFQSFPELGRSSRNVDLGAQYF 928
Db 897 HMEIFQFAFEVRSRNNYNTNLGSKPCF 925

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RESULT 6
US-09-738-269-57
; Sequence 57, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF

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; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-57

Query Match      40.1%; Score 1915; DB 12; Length 926;
Best Local Similarity 42.9%; Pred. No. 8.7e-135;
Matches 410; Conservative 156; Mismatches 333; Indels 56; Gaps 18;

QY 1 MKSFPKVFSTFAIFPLSM-----IATETVLDSSASFDGKNGNFSVRESQEDA 50
DB 1 MRSLYKILISSLTLPISFHSQHAELVLTQESILDA-----NGAFSPQSTSTAG 52

QY 51 GTTYLFGKNTVLENIPTGTATATKSCPNNTKGLDTFTGNGNSLLFQTVDAAGTAVAGAAVNS 110
DB 53 GTTYNVESDISIVDQ-QCTAALASSAFVQADNLTFKGNHSLITNANAG-ANPAGINV 110

QY 111 SVVDKSTFTFGFSLSPFASPGSSITTKGAVSCSTGSLTKNVSLLFSKNFSTDNCGA 170
DB 111 NTADKILTLTDFSKLSPKPCPSSLVNTGKGMK-SGGALNLANNASILFQNTSAENGGA 169

QY 171 ITAKTLTLTGTTSALPSENTSSKKGGAITQTSALITITGNQGEVSFSDNTSSDGAIFT 230
DB 170 ISCKAFSLTGSSEKISFTTNSTAKKGAIAATGIAHLSDNQGTIRFSGNTAVNSGGAVS 229

QY 231 EASVTISNNAKVPIDNKVTGASSTTGDMSGGAI CAYKSTSTDKVTLTGNOMLLFSNNT 290
DB 230 EASMTIAGNNHVAFNNNAVSGSS-----DCGGGAHCSKTGSAPTLLIRDNKVLIFEENT 284

QY 291 STTAGGAIYVKKLELASSGLTLFRSNVNGTAPKGAIAIEDSGELSLSDSGDIVFLG 350
DB 285 SSARKGGAITYDKLTLTSGGPTAFINNKVTHAT-PRGGAIGIAANGECSLTAHGDITFDN 343

QY 351 NTVTSTTTPGT-NRSSIDLGTSAKMTALRSAGRAIFYDPDITGSSSTTVTDVLKVNTPA 409
DB 344 NLMATQDNATIKRNAINEGKFNVLRAASGKTI SFYDPIITVEGN--AADLLTLNKAEG 401

QY 410 DSALQYTGNIIFTGEKLUSETAADSCKMLTSKLLQPVTLTSGGTLSLKHGVTLOQAFVQA 469
DB 402 DKT--YNGRIIFSGEKLTEEQAAVADNLKTTFTQPIITLAAGELVLRSGVEAEKTVVQTA 459

QY 470 DSRLEMDVGTLE-PADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTLTLDPT 528
DB 460 GSLILMDAGTKLSAKTADATLNLAINPNTLDGKFAVDVAAGKNTVLSGALGVIDPT 519

QY 529 GTFVENHSLRNPOQSVDILELAKSGTSTAVTPDPIIMG-EKPHYGYQGTWGPVW----- 582
DB 520 GKPHYENHKLNDLALGGIQLSGKSVTTTNV-PSHVVGVAETHYGYQGNWS-VSWVKDNN 577

QY 583 GTGASTATFNWTKTGYIPNPERIGSLVPNSLWAFIDISLHLVMEANEG-IQGBRAF 641
DB 578 SDPKTQTAIFTWNTKTYVNPERRAPLVNLSWGSFIDLRSIQVRLERSVDLSILETRGL 637

QY 642 WCAGLSNPFPHKDSKTRGFRHLSGGYVIGGNLHTCSDKILSAAPCOLFGDRDRDYFAKN 701
DB 638 WVSIGNFFHDKDRNAENKFRHISGVIYIGATTNFRSDLSVAPFCQFAKDKYLVSKN 697

QY 702 QGTVGGTLYYQHNTEYISL-----PCKLRPCSLSVPTTEIPVLFSGNLSYTHTDND 753
DB 698 AANYVAGSVYQHVSKFDDLTFLNPNPTC-----CSGFSKEIPIFLDAQITYCHTANN 751

QY 754 LKTYTTPYTVKSGWNSDFALEFGGRAPICLDSEALPEQMPFMKLOFVIAHQEGFKBQ 813
DB 752 MTTSTYDYPEVKGWNGDNLGTLTSTSVPIFVSSSIFDSYAPFAKLQVYVAHQDDFKEP 811

QY 814 GTEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTIGYTVDLVRSNPDCTTTILRISGD 873

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DB 812 TTEGRVFSSDLLNVSPIGIKPEKLSYCGERSAYDLTLMYIDPVYRHNPSMCTGLAINDV 871
QY 874 SWKTGNTLNRQALVLRAGNHCFNSNPFAPQSPFELRGSSRNYNVDLGAQVQF 928
DB 872 SWLTATNLARQAFIVRAGNHIALTSGVEMFQSGFELRSSRNYNVDLGAQVAF 926

RESULT 7
US-10-023-437-57
; Sequence 57, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS for Vaccination COMPRISING NUCLEIC ACI
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-57

Query Match      40.1%; Score 1915; DB 14; Length 926;
Best Local Similarity 42.9%; Pred. No. 8.7e-135;
Matches 410; Conservative 156; Mismatches 333; Indels 56; Gaps 18;

QY 1 MKSFPKVFSTFAIFPLSM-----IATETVLDSSASFDGKNGNFSVRESQEDA 50
DB 1 MRSLYKILISSLTLPISFHSQHAELVLTQESILDA-----NGAFSPQSTSTAG 52

QY 51 GTTYLFGKNTVLENIPTGTATATKSCPNNTKGLDTFTGNGNSLLFQTVDAAGTAVAGAAVNS 110
DB 53 GTTYNVESDISIVDQ-QCTAALASSAFVQADNLTFKGNHSLITNANAG-ANPAGINV 110

QY 111 SVVDKSTFTFGFSLSPFASPGSSITTKGAVSCSTGSLTKNVSLLFSKNFSTDNCGA 170
DB 111 NTADKILTLTDFSKLSPKPCPSSLVNTGKGMK-SGGALNLANNASILFQNTSAENGGA 169

QY 171 ITAKTLTLTGTTSALPSENTSSKKGGAITQTSALITITGNQGEVSFSDNTSSDGAIFT 230
DB 170 ISCKAFSLTGSSEKISFTTNSTAKKGAIAATGIAHLSDNQGTIRFSGNTAVNSGGAVS 229

QY 231 EASVTISNNAKVPIDNKVTGASSTTGDMSGGAI CAYKSTSTDKVTLTGNOMLLFSNNT 290
DB 230 EASMTIAGNNHVAFNNNAVSGSS-----DCGGGAHCSKTGSAPTLLIRDNKVLIFEENT 284

QY 291 STTAGGAIYVKKLELASSGLTLFRSNVNGTAPKGAIAIEDSGELSLSDSGDIVFLG 350
DB 285 SSARKGGAITYDKLTLTSGGPTAFINNKVTHAT-PRGGAIGIAANGECSLTAHGDITFDN 343

QY 351 NTVTSTTTPGT-NRSSIDLGTSAKMTALRSAGRAIFYDPDITGSSSTTVTDVLKVNTPA 409
DB 344 NLMATQDNATIKRNAINEGKFNVLRAASGKTI SFYDPIITVEGN--AADLLTLNKAEG 401

QY 410 DSALQYTGNIIFTGEKLUSETAADSCKMLTSKLLQPVTLTSGGTLSLKHGVTLOQAFVQA 469
DB 402 DKT--YNGRIIFSGEKLTEEQAAVADNLKTTFTQPIITLAAGELVLRSGVEAEKTVVQTA 459

QY 470 DSRLEMDVGTLE-PADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTLTLDPT 528
DB 460 GSLILMDAGTKLSAKTADATLNLAINPNTLDGKFAVDVAAGKNTVLSGALGVIDPT 519

QY 529 GTFVENHSLRNPOQSVDILELAKSGTSTAVTPDPIIMG-EKPHYGYQGTWGPVW----- 582

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Db 520 GKFEYENKLANDTLALGQIOLSGKSGSVTTNN-PSHVVGVAETHYGYQGNWS-VSWVKDNN 577
Qy 583 GTGASTTATENWTGTGVPINPERIGSLVPNSLWNAFIDISLHLYMETANEG-LQGDRAF 641
Db 578 SDPTQTQTAIFWNTKGTGVPINPERAPLVLNLSWGSFIDLSRIQDVLERSVDLSILETRGL 637
Qy 642 WCAGLSNFFPHKDSKTTRGPHRLSGGVYVGNLHSCDKLSAAPCOLFGDRDRYFVAKN 701
Db 638 WUSGIGNFFHKDRNAENRKPRISSGYVLGATTINTSREDSLSVAFCOLFAKDKDYLVSKN 697
Qy 702 QGTVYGGTLYYQHNETYISL-----PKLRPCSLSYVTEPVLPSGNLSYTHTDND 753
Db 698 AANYAGSVYQHVSKFDLTLFLNGPNTC-----CSGFSKEIPILDAQITCYHTANN 751
Qy 754 LKTYTTPYTVKSGWGNDSFALEFGGRAPICLDESALFEQWMPFMKLOFVYAHQEGFKEQ 813
Db 752 MTSYTDYPEVKGWGNDDTLGLTSTVPIPVFSSIFDSYAPAKLOVVYAHQDDFKEP 811
Qy 814 GTEAREFGSSRLVNLALPIGIRFDKESQCDATYNLTGYTVDLVRSNPDCTTLIRISGD 873
Db 812 TTEGRVPSSDLLNVSVBIGIKFEKLSYGRSAYDLTLNYPDVYRHNPSQMTGLAINDV 871
Qy 874 SWKTFGTNLARQALVLRAGNHCFSNFEAFSOFSEFELRGSSRNYNVDLGAKYQF 928
Db 872 SWLTATNLARQAFIVRAGNHIALTSVGMFESQFELRGSSRNYNVDLGAKVAF 926

RESULT 8
US-09-738-269-23
; Sequence 23, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; FILE REFERENCE: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-23

Query Match 34.7%; Score 1656.5; DB 12; Length 839;
Best Local Similarity 40.3%; Pred. No. 1.8e-115;
Matches 381; Conservative 133; Mismatches 285; Indels 147; Gaps 24;

Qy 11 STFAIPPLSMI-ATETVLSSASFDGN-KGNFSVRESQEDAGTTLYFKGNVLENIPTG 68
Db 13 SLFASNSLSPANDAQTALTPSDSYNGNVTSEFQVKET--SSGTTTTCGNVCI-SFAGK 69
Qy 69 GTAITKSCFNNTKGLTFTGNGSLPQTVDAGTVAGAAVNSVVDKSTFFIGFSSLSFI 128
Db 70 DSGLLKSCFSAT-DNLTFLNGVYTLCPDNITTTASNPAGINVOGQKTLGISGSLFSCA 128
Qy 129 ASPGSSITTKGAVSCSTGSLSTKNVSLFKNFSTDNAGAITAKTSLTGTMTSALFS 188
Db 129 YCPGP--TTGVALQ-TKGNITLKDSSLVFKHNCSTAEAGAIQC----- 170
Qy 189 ENTSSKKGAIQTSALDITIGNQGEVSFSNTSSDGAALFTEASVTISNNAKVSIIDNK 248
Db 171 ----- 170
Qy 249 VTGASSSTTGDMSSGALCAVKTSTDKVTLTGQMLLFSNNTSTTAGGAIYVKKLELASG 308

Db 171 -----KGSSDAELKIENNQNLFVSENSSTSKGAIYADKLATIVSG 210
Qy 309 GLTLFRNSVNGTAPKGAIAIED-SGELSLSADSGDIVFLGNTVTSITPGIN---RSS 364
Db 211 GPTLFNNSVNSGSSPKGGAISIKDSGSCSLADLGDITFDGNKIKTSGGSSTVTRNS 270
Qy 365 IDLGTSAKMTALSAAGRAIFYDPITTTGSSSTTVTVLKVNETPADSALQYTGNIIFTGE 424
Db 271 IDLGT-GKFTKLAKOGFGIFFYDPITGGG-----DELNINK---KETVDYTKIVFSGE 322
Qy 425 KLSETEADSKNLTSLKLPVLTSGGTLKLGHTVLTQTAFTQQAOSRLMDVGTTLLEP- 483
Db 323 KLSDEEKARAEENLASTFNQPIITLSAGSLVLKDGVSVTAKQVTOEAGSTVVMDLGTLTQTP 382
Qy 484 ---ADTSTINNLVINISSI---DGAKKAKIETKATSKNLTSLGTTITLLDPTGFYENHSL 537
Db 383 SSGGETITTLNLDINIASLGGGGTSPAKLATNTASQAITIN-AVNLDVADGNAEYDPIIL 441
Qy 538 RNPOSYDILBLKASGTVTSTAVIDPIMPGE---KFHYGYQGTWGPVIMVGTGAST-TATFN 593
Db 442 ATSEFTAI---VATTNASTVTPQTDNLTVNVPPTHYGYQGNW-TVTDIETATKATLT 497
Qy 594 WTKTGYIPNPERIGSLVPNSLWNAFIDISLHLYMETANEGLOCDRAFWCAGLSNFFHKD 653
Db 498 WEQTGYSPNPERQGPLVENTILWGAFLRAITONLMDISVNGADYHRCGFVWSGLANFLHKS 557
Qy 654 STKTRGFRHLSCGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNOGTVYGGTLYYQ 713
Db 558 GSDTKRFRHNSAGYALGVYAKTSPDDIFSAFCQLFGKDKDYLVSNNANIYAGSLYYQ 617
Qy 714 HNETYISLPCKLRPCSLSYVTEIPVLPSGNLSYTHTDNLT-----KYTTYPTVK 765
Db 618 H-----ISYWSAQNLQNTIGAEAPVLVNAQLTYCHASNDMKTNTTTPYAPKTTYAEIK 673
Qy 766 GSWGNDSPALEFGGRAPICLDESALFEQWMPFMKLOFVYAHQEGFKEGT-EAREFGSSR 824
Db 674 GDWGNDCFGVELGATVPIQTSSLLFDWYSPFLKFLVHTHQDDFKENNSDQGRYFESSN 733
Qy 825 LVNLALPIGIRFDKESQCDATYNLTGYTVDLVRSNPDCTTLIRISGDS--WKTFTGNL 882
Db 734 LTNLSLPIGIRFERPANNDTASYHVTAAYSPDIVRSNPDCTTSLLVSPDSAVWVTKANL 793
Qy 883 ARQALVLRAGNHCFSNFEAFSOFSEFELRGSSRNYNVDLGAKYQF 928
Db 794 ARSAFMLQAGNYLSLHSHIEIFSGFELRGSSRNYNVDLGSKIOF 839

RESULT 9
US-10-023-437-23
; Sequence 23, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC AC
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-23

Query Match 34.7%; Score 1656.5; DB 14; Length 839;
Best Local Similarity 40.3%; Pred. No. 1.8e-115;

```
Matches 381; Conservative 133; Mismatches 285; Indels 147; Gaps 24;
11 STEAIFPLSMI--ATETVLDSSAFQGN--KGNFNSVRESQEDAGTTLFKGNVTLENIPGT 68
13 SLFASNSLSFANDAQTALTPDSYNGNVTSEFQVKE--SSGTTYTCEGNVCI--SPAGK 69
69 GTAITKSCFNNTKGDLTFTGNNSLLPOTVDAGTVAGAAVNSVVDKSTFTFGFSSLFPI 128
70 DSGLLKSCFSAT--DNLTFNGNITLCFDNITTAAGNAINVQOGQKTLGIGSFLFSCA 128
129 ASPGSSITTKGAVSCSTGSLTKNVSLLFKNFSTDNCGAIAITAKTSLTGTWMSALFS 188
129 YCPGP--TTGYGAIQ--TKGNTTLKONSLVFKNCSTABGAIQC----- 170
189 ENTSSKKGAIQTSDALTTITGNQGEVFSFSDNTSSDGAIAIFTEASVTISNNAKVFDINK 248
171 ----- 170
249 VTGASSITGDMGGGAI CAYKSTDTKVTLTGNOMLLFSNNTSTTAGGAIYVKKLELASG 308
171 -----KGSDAELKIENNQNLFSENSTSGKGAIIYADKLTVSG 210
309 GLTLFERNVNGTAPKGAIAIED--SGBELSADSGLDIVFLGNTVTSTPGTN---RS 364
211 GPTLFNNNSVNGSPKGAISIKDSGRCSLTADLGDITFDGNKIITSGGSSTVTRNS 270
365 IDLGTSAKMTALRSAAAGAIYFVDPTTGGSTTVTVLKVNETPADSALOYTCNIIPTGE 424
271 IDLGT--GKFTKLRAKDGFGFFDPTTGGGS-----DELINK---KETVDYTGKIVFSGE 322
425 KLSSETAASKNLTSKLLQPVTLSGTSLIKHGVTLOQTAFTQOADSRLMDVGTLEP-- 483
323 KLSDEEKAENLSTFNPOTILSAGSLVKQGVTAQVTOEAGSTVVMDLGTLTLOTP 382
484 ---ADSTNNLVINISSI---DGAKAKIETKATSKNLTSLGCTITLLDPTGTFFYENHSL 537
383 SSGGEITLTNLDINIASLGGGGTSPAKLATNTASQAITN--AVNLVDADGNAYEDPIL 441
538 RNPQSDVILELKASGTVTSTAVTPDPMGE---KPHYGQGTWGPVWGTGAST--TATFN 593
442 ATSKPFTAI---VATTNASTVTQTDNLNTNVVPPTHYGYQGNW--TVTMDTETATKTALT 497
594 WTKGTGIPNPERIGSLVPSNLWAFIDISLHLYMETANEGLQDRAFCAGLSNPFHKD 653
498 WEQTGSPNPEROGPLVENTLWAFSDLRATONLMDISLVNGADYHGRFVWSGLANFLHKS 557
654 STKTRRGFRHLSGGYVIGGNLHSCDKILSAAFCQLFGRDRDYFAVAKNQGTVYGGTLYYQ 713
558 GSDTKKFRNSAGYALGVYAKTPSDDI FSAAFQCLFGKDKDYLVSNNANIYAGSLYYQ 617
714 HNBTYISLPCKLAPCSLSYVPTTELPVLPSGNLSYTHTDNDLKT-----KYTTYPTVK 765
618 H---ISYSAWQMLLQNTICAEAPLVNLAQLTYCHASNMDKNTMTTYAPRKTYYAEIK 673
766 GSGWNSDALEFGGRAPICLDESALPEQYMPFKLPVYAHQSGFKQGT--BAREFGSSR 824
674 GDMWNCFGVELGATVPIQTESLSLFDMYSEFLKPLVHTHQDDFKENNSDQGRYFESSN 733
825 LVNLALPIGRFHKESDCODATVNLTLGYTVDLVRSNPDCTTIRISGDS--WKTFTNL 882
734 LTNLSLPIGIKFERFANNRTASYHTVTAAYSPDIVRSNPDCTTSLVSPDSAAVWTKANNL 793
883 ARQALVLRAGNHCFNENFEAFQSFPELGRSSRYNVVDLGAKYQF 928
794 ARSAFMLQAGNLSLHSHNIBIFSQGFELGRSSRTYVNDLGSKIQF 839
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RESULT 10

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US-09-886-468-19
; Sequence 19, Application US/09886468
; Patent No. US20020037293A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pasteur Limited
```

```
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the:
; FILE REFERENCE: 77813-5
; CURRENT APPLICATION NUMBER: US/09/886,468
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,280
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,281
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,282
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,283
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,284
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,285
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,385
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114,050
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,056
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,057
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,058
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,059
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,061
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-886-468-19
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Query Match 30.1%; Score 1437.5; DB 9; Length 922;
Best Local Similarity 36.8%; Pred. No. 5.6e-99;
Matches 350; Conservative 156; Mismatches 382; Indels 63; Gaps 26;
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QY 5 FP-KFVFSTFAIFPLPSMIATETVLDSSAFQGNKGNFNSVRESQEDAGTTLFKGNVTLE 63
DB 8 FPLVFSFLLSVFDTLSLATTISLTPEDSFHGDSQN--AERSNVVQAGDVYSLTGDVSL 65
QY 64 NIPGTGTAITKSCFNNTKGDLTFTGNNSLLPOTVDAGTVAGAAVNSVVDKSTT-FIGF 122
DB 66 NV--DNSALNKACFNVTSGSVTFAGNHGGLYFNNTISSGTTKGAVALCCQDPQATAPSGF 123
QY 123 SLSLPTASPGSSITTTCKGAVSC--STGSLSTQNVSLLFSKNPSTDNCGAIAITAKTSLTGT 180
DB 124 STLSFQSPGDIKEQG-----CLYSKNALMLNNVYVRFQGNQSKTKGAISGANTVIG 178
QY 181 TTMSALFSENTSKKGAIQTSDALTTITGNQGEVFSFSDNTSSD--SGAIAIFTEASVTISNN 239
DB 179 NYDSVSPYQNAAT--FGAIIHSSGPIQIAVNOABIREAQNATKNGSGALYSDGDIIDQN 237
QY 240 AKVSPFDNKVTVGASSSTTGMDSGGAICAYKSTDTK-----VTLTGOMLLFSNNTSTTAG 295
DB 238 AYLFLFRENE-----ALTTAIGKGGAVCCLPSTGSSSTPVPITVTFSDNKLVLFEHNHIMG 292
QY 296 GAIYVKKLELASGLTLFERNVNGTAPKGAIAIEDSGELSLSDSADSGDIVFLGNTVTS 355
DB 293 GAIYARKLSISSGGPTLFINNISYANSONLGAIAIDTGGELISLBAKGTIITQGN--RT 350
QY 356 TTPGTNRSSIDLGTSAKMTALRSAAAGAIYFVDPTTGGSTTVTVLKVNETPADSALOY 415
DB 351 SLFPLN--GHLLQNAKFLKLAQNGVSYIEFYDPI--SEADGSTQLNINGDPKNC--EY 404
QY 416 TGNIIFTGEKLSSETAADSKNLTSKLLQPVTLGGTSLSKHGVTLOQTAFTQOADSRLM 475
DB 405 TGTILFSGEK---SLANDPRDFKSTTIPQNVNLGAGVIVIKEGAETVTSKFTQSPGSHVL 461
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Db 580 VANTLWNTYSDMQAVQSMINTTAHG--GAYLFTGWSAVSNLFYVHDSGSKPIDNWHRS 637
QY 666 GGVVIGGNLHTCSDKILSAFQCFGRDRDYFVAKNQGTGYGGLYYQHNETYISLPCKL 725
Db 638 LGVLFGISHTSLDDHSCFLAAGQLLKSSDSFITSITTSYIATVQAQLATSLMKI--- 693
QY 726 RPCSLSYVTEIPVLPFSGNLSYTHTDNLTKYTYPTVK-GSWGNDSPALFPGGRAPIC 784
Db 694 -----SAQACYNESIHLEKTKYRSFSGEGFSGWSHVAVSVEVCASIPIV 737
QY 785 LDESALFEQYMPFMKLFVYAHQEGKEQTEAREFSGSRLVNLALPIGRPOKESDCOD 844
Db 738 SNGSGLFSSFSIFSKLQFSGTQDGFEESSGEIRSFSSASFRNISLPIGITFEKKSQ-KT 796
QY 845 ATYNLTIG-YTVDLVRNPDCTTTLRISGDSWKTFTGNLARQALVLRAGNHFCFNSNFEA 903
Db 797 RTYYFLGAYIQDLKRDVESGPVLLKNVAVSWDAPMANLDSRAYMFLTNQRALH-RLQT 855
QY 904 FSQFSFELGSSRNYNVDLCAKYOF 928
Db 856 LLNVSCVLRQSHSYSLDLGTTYRF 880

RESULT 14
US-09-841-132-189
; Sequence 189, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 189
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Chlamydia
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(866)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-189

Query Match 17.9%; Score 856; DB 9; Length 866;
Best Local Similarity 30.1%; Pred. No. 2.1e-55;
Matches 260; Conservative 123; Mismatches 368; Indels 114; Gaps 24;
QY 118 TFIGSSLSFIASPGSSITTKGAVS-----CST-----GSLSLTKN 154
Db 62 SYCFVSKLHTDPKALFKKGLDLSIQNFRFLFTDCSSKSSPSIITHQKNGLSLNN 121
QY 155 VSLFSKRNFTDNGGAIKTAKTSLSLGTMTMSALFSENTSKKGGAIQTSALTITGNQGEV 214
Db 122 GMSFCRNHAEGSGGAIADAFSLQHNLYLFTAFENSKGNGGAIQ-AQTFSLSRNVSPI 180
QY 215 SPSDNTSSDGAATEASVTISNNAKVSFDINKVTGASSSTTGMSSGAICA---YKTS 271
Db 181 SPARNRADLNGAICCSNLICSGNVPNPLFTGNSAT-----NGXICISDLNLS 230
QY 272 TDTKVTLCNOMLLFSNNSTTTAGGAIYVKKLEASGLTLFNRSNVNGTAPKGAIAI 331
Db 231 EKGSLSLACNQTLTASNAKKGKGAIVAKHVLVNGVPVSFINNS-----AKIGGAIAI 285
QY 332 EDGSLSLADSAGDIVFLGNTVTTSTPGTNRSSIDLGTSAKMTALRSAGRIAYPDPI 391
Db 286 QSGGSLSLAGSGVLFOQNSQRTSDQGLVRNVAILEKDAILSLSEARNG-DILFPDPI 344

QY 392 TGSSTTVTDVLKVNTPADSLQY-----GNIIFTGKLSSETAA 432
Db 345 QESS-----KESPLSSLOASVTPTATASPLVIQTSANRSVIFSSRLSEBEKT 396
QY 433 DSKNLTSLKLPVTLGGTSLKKGVTIQTQAFQOASRLMDVGTTLLEPADTSTINNL 492
Db 397 PD-NLTSLOQFIELKSGRLVLDRAVLSPSLSDPQALLTMEAGTSLKTSXDLKLTXTX 455
QY 493 VINISIDGAKAKATETKATSKNLTSLGTITLLDPTGFYENHSLRNQSYDILELKASG 552
Db 456 SIPLHSLDTEKSVTH-----APNLSIQKIFLNSGSDENFYENVLLSKENNI-PLLTLP 510
QY 553 TWTSTAVTPDPIGMEKFHYGYQTWGPVW---GTGASTTATFNMTKTGYIENPERIGSL 609
Db 511 KQCSHLHLPDGNLSS--HFGYQGDW-TFSWKDSDEGHSLIA--NWTPKNVVPHPERQSTL 565
QY 610 VPNSLWNAFIDTSSILHYLMETANEGLQGDRAF--WCAGLSNFF--HKDSTKTRRGRHLS 665
Db 566 VANTLWNTYSDMQAVQSMINTTAHG--GAYLFTGWSAVSNLFYVHDSGSKPIDNWHRS 623
QY 666 GGVVIGGNLHTCSDKILSAFQCFGRDRDYFVAKNQGTGYGGLYYQHNETYISLPCKL 725
Db 624 LGVLFGISHTSLDDHSCFLAAGQLLKSSDSFITSITTSYIATVQAQLATSLMKI--- 679
QY 726 RPCSLSYVTEIPVLPFSGNLSYTHTDNLTKYTYPTVK-GSWGNDSPALFPGGRAPIC 784
Db 680 -----SAQACYNESIHLEKTKYRSFSGEGFSGWSHVAVSVEVCASIPIV 723
QY 785 LDESALFEQYMPFMKLFVYAHQEGKEQTEAREFSGSRLVNLALPIGRPOKESDCOD 844
Db 724 SNGSGLFSSFSIFSKLQFSGTQDGFEESSGEIRSFSSASFRNISLPIGITFEKKSQ-KT 782
QY 845 ATYNLTIG-YTVDLVRNPDCTTTLRISGDSWKTFTGNLARQALVLRAGNHFCFNSNFEA 903
Db 783 RTYYFLGAYIQDLKRDVESGPVLLKNVAVSWDAPMANLDSRAYMFLTNQRALH-RLQT 841
QY 904 FSQFSFELGSSRNYNVDLCAKYOF 928
Db 842 LLNVSCVLRQSHSYSLDLGTTYRF 866

RESULT 15
US-09-738-269-53
; Sequence 53, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-53

Query Match 17.8%; Score 851.5; DB 12; Length 679;
Best Local Similarity 30.9%; Pred. No. 3.2e-55;
Matches 243; Conservative 116; Mismatches 283; Indels 145; Gaps 23;
QY 1 MKSS-FPKVFSTFAIPLS-MIATEVTLDSSASFDGKNGKNGFVSRESQEDAGTTLFKG 58
Db 6 MKNISYGVLLFSLPSTATKLLADASVNLATFNGSTSTFNNKQTDNADGTYILGS 65
QY 59 NVTLENIPGTGTATKSCFNNTKGLDFTFTGNLGLLFTQVDAGTVAGAAVNSVVDKSTT 118

Db	66	AITFEHNLQKPANT-SCFANTAGDLTFTGNRRLLYFNNI--SSTAKGAIAISTTACKTLT	123
Qy	119	FIGFSSLSFIASPGSSIITTKGAVSCSTGSLTKNVSLLFSKNFSTDGGCAITAKTILSL	178
Db	124	ISGALQLIFYMSP--RLATNG-	143
Qy	179	TGTTMSALFSENTSKKGGAIQTSDALVITNQGEVFSFDMTSSDGAIAIFTEASVTISN	238
Db	144	-----VIYSSNVLLEN	155
Qy	239	NAKVSFIDNKVGTGASSSTTGDMSGGAI CAYKTTSTDKVT-----LTGNQLLFSNNTST	293
Db	156	NSQSSGLNKSA- - - - - KGVPICEK- STDVGAITSPTLIRNNGEFTLVGNATS	205
Qy	294	AGGAIYVKKLBSLGGTLTFFORNVSNGGTAPKGGAAIAIEDGGEISLSDAGSDIVFLGNTV	353
Db	206	SGGAIYAEKMTLSGGVYTKFQSNV-----SYDQGAIAIAPNGEISLSDAKGNIVERNLK	261
Qy	354	TSITPGINRSSIDIGTSAKMTALRSAAAGRAIYFYDPITTGSTTTVDVLKUNETPADSAL	413
Db	262	IANKQNT--PNAIHGLGDNAKFLQLRAANNKAIFYDPITTTGS--VADRLIINNSQGE--AS	317
Qy	414	QYTGNIITFGEKLSETEAAADSKNLTSLKLPQVTLSCGTLSLKHGVTLOTQAFTOQADSR	473
Db	318	TYDGAIVFSSLNLF-THSPECK--LSSFSQGLTLAAGSLVLEEGVCVQAPSFQRAHSQ	374
Qy	474	EMDVGTTLEPADTGTINNLVINISIDGAKKAKIETKATSKNLTLSGTLTLLDPTGTFTYE	533
Db	375	FMPNPGTKLQATQNISVKNLHLNRI-AEEPAIYITTTDDASSVDICGPVVMHIDEIFYN	433
Qy	534	NHSLRNQSYDILKAS--GTVITSTATPPDPMGEKHEHYGYOGTWGPVWGCT-----G	585
Db	434	QTVJANELLVBECLNLSLPHLDNIITDDVPVIMTLESHRGYGGTW-EISWKEQKPLFG	492
Qy	586	ASTTAT-----FNTKTYIP-----NPBRIGSLVPNSLWNAPIDISLHYLMETANEGLQ	636
Db	493	KATIAPNKQMHLIWKPSGYVFPFGSGTGFTTSLVPNSLWNLFLDRFSQAIE--KHAVS	550
Qy	637	GDRAWCAGLSNPHKOSTKTRGPRPHSGGVVIGCNLHTCSDKILSAAPCOLFGDRD	696
Db	551	SGNGIWISSMTNSFLQSGTNNNHGPRHXSOGYTAGGKIQTLLQDDIFSVSFSOLFGRSKD	610
Qy	697	FVAKNOGVYGGTLYYQHNE-----TVISLPCKLRPCSLSVVPEIPLVPSGNLSYTH	750
Db	611	GSATSKDTFLSGSIYAQHSRLLPIMRFLAGTSTYRPRLLISIPKXNLFINFVLVSYSD	670
Qy	751	DNDLTKT	757
Db	671	SNHMKVO	677

Search completed: December 16, 2003, 10:59:53
Job time : 40 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 10:49:50 ; Search time 27 Seconds
(without alignments)
3305.353 Million cell updates/sec

Title: US-09-428-122-2
Perfect score: 4774
Sequence: 1 MKSSFPKVFSTFAIFPLSM.....FELGSSRNYYNDLGAKYQF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3991	83.6	772	H86492	Pmp_3 [imported]
2	2058	43.1	928	G86546	polymorphic outer
3	2058	43.1	928	G81591	polymorphic membra
4	1982	41.5	928	B86546	polymorphic outer
5	1982	41.5	928	B72077	polymorphic membra
6	1965	41.2	936	C72078	polymorphic outer
7	1964	41.1	936	C86546	polymorphic outer
8	1964	41.1	936	B81591	polymorphic membra
9	1940	40.6	930	D86546	polymorphic outer
10	1940	40.6	930	A81591	polymorphic membra
11	1936	40.6	930	D72078	polymorphic outer
12	1855	38.9	928	H86546	polymorphic outer
13	1855	38.9	928	D72077	polymorphic outer
14	1855	38.9	949	F81591	polymorphic membra
15	1573	32.9	841	E72130	polymorphic outer
16	1444	30.2	1276	B86546	polymorphic membra
17	1444	30.2	1276	C81591	polymorphic outer
18	1442.5	30.2	922	B72131	polymorphic membra
19	1442.5	30.2	922	E86491	polymorphic outer
20	1441.5	30.2	922	F81539	polymorphic membra
21	1383.5	29.0	1407	B72078	polymorphic outer
22	1377.5	28.9	973	B86547	polymorphic membra
23	1377.5	28.9	973	F72076	polymorphic outer
24	1377.5	28.9	995	C81593	polymorphic membra
25	1246	26.1	712	E86492	polymorphic outer
26	1120.5	23.5	1013	G71460	probable outer mem
27	1051	22.0	987	H81722	polymorphic membra
28	1017.5	21.3	445	E86493	Pmp_5 [imported]
29	916	19.2	359	C86493	Pmp_4 [imported]

30	911	19.1	867	2	F81721	polymorphic membra
31	863	18.1	878	2	B71460	probable outer mem
32	821	17.2	494	2	D86493	polymorphic outer
33	792	16.6	427	2	A86493	polymorphic outer
34	768	16.1	186	2	G86492	polymorphic outer
35	685.5	14.4	1609	2	A86611	probable outer mem
36	685.5	14.4	1609	2	H72013	polymorphic membra
37	672.5	14.1	978	2	G72076	polymorphic outer
38	670	14.0	947	2	G86557	polymorphic outer
39	667.5	14.0	978	2	B81593	polymorphic membra
40	667.5	14.0	978	2	C86547	polymorphic outer
41	666	14.0	947	2	D72067	polymorphic membra
42	666	14.0	1723	2	H86557	polymorphic membra
43	666	14.0	1723	2	E72067	polymorphic membra
44	666	14.0	1732	2	C81601	polymorphic membra
45	665.5	13.9	946	2	C86549	polymorphic outer

RESULT 1
H86492
Pmp_3 [imported] - Chlamydothila pneumoniae (strain J138)
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: H86492
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: H86492
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-772 <STO>
A:Cross-references: GB:BA000008; NID:g8978389; PIDN:BAA98226.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_3_2

Query Match		83.6%	Score 3991;	DB 2;	Length 772;
Best Local Similarity		99.9%	Pred. No. 2.3e-208;		
Matches 771;		Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	157	LLFSKNFSTDNCGAITAKTSLTGTMTSALFSENSSKKGAIQTSDALTTGNQGEVSF	216		
DB	1	MLFSKNFSTDNCGAITAKTSLTGTMTSALFSENSSKKGAIQTSDALTTGNQGEVSF	60		
QY	217	SNTSSDSGAALFTEASVTISNNAKVSFDNKVTGASSTTGDMSGGAIQVKTSTDTKV	276		
DB	61	SNTSSDSGAALFTEASVTISNNAKVSFDNKVTGASSTTGDMSGGAIQVKTSTDTKV	120		
QY	277	TLTGNQMLFSSNNTSTTAGGAIYVKKLELASGGLTLFSENSSVNGGTAPKGGAIATEDSGE	336		
DB	121	TLTGNQMLFSSNNTSTTAGGAIYVKKLELASGGLTLFSENSSVNGGTAPKGGAIATEDSGE	180		
QY	337	LSLSADSGDIVFLGNTVSTTGTNRSSIDLGTSAKMTALRSAAAGRAIYFYDPTTGSST	396		
DB	181	LSLSADSGDIVFLGNTVSTTGTNRSSIDLGTSAKMTALRSAAAGRAIYFYDPTTGSST	240		
QY	397	TVIDVLKVNETPADSALQVGTGNIIFTGEKLSATEAASDKNLSKLLQVTLSSGGLSLKH	456		
DB	241	TVIDVLKVNETPADSALQVGTGNIIFTGEKLSATEAASDKNLSKLLQVTLSSGGLSLKH	300		
QY	457	GVTLTQTAFTQADSRLMDVGTTLTLEPADTSTINNLVINISSIDGAKAKIETKATSKNL	516		
DB	301	GVTLTQTAFTQADSRLMDVGTTLTLEPADTSTINNLVINISSIDGAKAKIETKATSKNL	360		
QY	517	TLUSGHTLLDPTGTTFYENHSLRNPOSIDILELKASGTVTSTAVTTPDPMGEKHYGYQQT	576		
DB	361	TLUSGHTLLDPTGTTFYENHSLRNPOSIDILELKASGTVTSTAVTTPDPMGEKHYGYQQT	420		
QY	577	WGPIVWGTGASTATFNTKTYIPNPERIGSLVPSNLWNATFIDISSLHYLMETANEGLQ	636		

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|||||
Db 421 WGPVWGTAATATFNWTKGYPNPERIGSLVPSNLWNAFIDISLHVLMTANEGLQ 480
QY 637 GDRAFWCAGLSNPFHKDSTKTRGFRHLGSGYVIGNHLTCSDKILSAAPCOLFGRDRDY 696
Db 481 GDRAFWCAGLSNPFHKDSTKTRGFRHLGSGYVIGNHLTCSDKILSAAPCOLFGRDRDY 540
QY 697 FVAKNOGTVVGGLTYOHNETHYISLCKLRPCSLSYVPTPIPLVFSGNLSYTHTDNDLKT 756
Db 541 FVAKNOGTVVGGLTYOHNETHYISLCKLRPCSLSYVPTPIPLVFSGNLSYTHTDNDLKT 600
QY 757 KYTTPYTVKSGWNGDSFALFEGGRAPICLDESALFEQYMPFMKLQFYVAHQEGFKEQGT 816
Db 601 KYTTPYTVKSGWNGDSFALFEGGRAPICLDESALFEQYMPFMKLQFYVAHQEGFKEQGT 660
QY 817 AREFGSSRLVNLALPIGIRDFKESDCQDATYNTLGTVDLVRNPDCTTTLRISGDSWK 876
Db 661 AREFGSSRLVNLALPIGIRDFKESDCQDATYNTLGTVDLVRNPDCTTTLRISGDSWK 720
QY 877 TFGTNLARQALVLRAGNHFCFNSNFEAFSOFSPELGRSSRNYNVDLGAKYQF 928
Db 721 TFGTNLARQALVLRAGNHFCFNSNFEAFSOFSPELGRSSRNYNVDLGAKYQF 772

RESULT 2
G86546
polymorphic outer membrane protein G family [imported] - Chlamydomophila pneumoniae (strain
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: G86546
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <STO>
A;Cross-references: GB:BA000008; NID:g8978821; PIDN:BA98657.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp 10
C;Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSFFPKFVP-STFAIF---PLSMIATETVLDSSASFDGNKN-GNFSVRSEQEDAGTYL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFATAENIGPSDFDGTNTGTYTPKNT--TTGIDYT 58
QY 56 FKNVTLENIPGCTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAGAANSSVVDK 115
Db 59 LTGDITLQNL-GDSAALTGKCFSDTTESLFAKGYSLFLNKS-SAEGAAL-SVTTDK 115
QY 116 STTFIFGSSLSFIASPGSSITTT--GKAVSCSTGSLTKNVSLFSKFNSTNGGAITA 173
Db 116 NLSLTGSSSTFLAAPSIVITPSGKAVKCG-GDITFDNNHTILFKQDYCEENGGAIST 174
QY 174 KTLSLTGTTMSALFSENSTSS---KKGAIQTSDALITIGNQGEVFSFSDNTSSDSGGAIFT 230
Db 175 KNLSLKNTGSISEFGNKSATGKGGAI CATGTVDTTNTATPLFSNNTAEEAGGAINS 234
QY 231 EASVTIENNAKVPIDNKVTTGASSSTTGDMSGGAICAYKSTSTDKVTLTGQMLLSNNT 290
Db 235 TGNCTITGNTSLFSENSVT---ATAG--NGGAL-----SGDADVTISGNQSVTFSGNQ 283
QY 291 STTAGGAIYVKKLELAS--GGTLTFLSNSVNGGTAPKGGAIADSDGELSADSGDIVF 348
Db 284 AVANGGAIYAKKUTLASGGGGGSIFFSNIVQGTAGNGGAISILAAGECSLSAEAGDITF 343
QY 349 LGNTVTISTTP-GTNRSSIDLGTSAKMTALRSAGRAIYFYDPIITGSSITTVTDVLKNET 407
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|||||
Db 344 NGNAIVATTPTQTKRNSIDIGSTAKITNLRALSGHSIFFIDPITANTAADSTDTLNLNKA 403
QY 408 PADSALOYTGNITIFTGEKLSSEADSKNLTSLKLPVTLSGGTLSLKHGVTLTQOAFQ 467
Db 404 DAGNSTDYSGSIVFSGEKLSSEADSKNLTSLKLPVTLSGGTLSLKHGVTLTQOAFQ 463
QY 468 QADSRLEMDVGTLEPA-DTSTINNVLINISIDGAKKAKIETKATSKNLTJSGTITLLD 526
Db 464 TAGSSVIMDAGTTLKASTEVEVTLTGLSIPVDSLGEKGVVIAAASAKNVALSGPILLD 523
QY 527 PTGTFVNHSLRNPOSYDITLKLKASQTVTSTAVTPDIPMGERKPHYGYQGTWGPVW---- 582
Db 524 NQGNAYENHDLGKTQDFSFVQLSALGTATTVDPAVPTVATPTHGYQGTWGTWVDDT 582
QY 583 -GTGASTTATFNWTKGYIPNPERIGSLVPSNLWNAFIDISLHVLMTANEGLQDRAF 641
Db 583 ASTPKTKTATLAWNTGVLNPERQGPLVPSNLWNGSFSDIQAIQGVIERALSALTLCSDRGF 642
QY 642 WCAGLSNPFHKDSTKTRGFRHLGSGYVIGNHLTCSDKILSAAPCOLFGRDRDYFAKN 701
Db 643 WAAGVANFLDKDKGKRYRHKSGGYAIGGAAQTCSNLISFAFCQLFGSDKDFLVAKN 702
QY 702 QGTVYGGTLYOHNETHYISLCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKY 758
Db 703 HDTYAGAFYIQH---ITECSGFCGLDLDKLPGWSHAPLVLEGLAYSHVNSNDLTKY 758
QY 759 TYTTPYTVKSGWNGDSFALFEGGRAPICLDESALFEQYMPFMKLQFYVAHQEGFKEQGT 818
Db 759 TAYPEVKGSGWNGNAFNMGLGASSHSYPEYLHCFDTPYVYKLNLTVIRQDSFSEKTEGR 818
QY 819 EGSRLVNLALPIGIRDFKESDCQDATYNTLGTVDLVRNPDCTTTLRISGDSWKTF 878
Db 819 SFDDSNLFLNLSPIGVKFEKSDCNDFSYDLTSLVYVPLIRNDPKCTTALVISGASWET 878
QY 879 GTNLARQALVLRAGNHFCFNSNFEAFSOFSPELGRSSRNYNVDLGAKYQF 928
Db 879 ANNLRQALQVRAGSHYAFSPMFEVLQGVFVGRSSRNYNVDLGKQFQF 928

RESULT 3
G81591
polymorphic membrane protein G family CP0303 [imported] - Chlamydomophila pneumoniae (
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C;Accession: G81591
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hick
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR3
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: G81591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-928 <REA>
A;Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38160.1; PID:g71
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0303
C;Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSFFPKFVP-STFAIF---PLSMIATETVLDSSASFDGNKN-GNFSVRSEQEDAGTYL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFATAENIGPSDFDGTNTGTYTPKNT--TTGIDYT 58
QY 56 FKNVTLENIPGCTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAGAANSSVVDK 115
Db 59 LTGDITLQNL-GDSAALTGKCFSDTTESLFAKGYSLFLNKS-SAEGAAL-SVTTDK 115
QY 116 STTFIFGSSLSFIASPGSSITTT--GKAVSCSTGSLTKNVSLFSKFNSTNGGAITA 173
Db 116 NLSLTGSSSTFLAAPSIVITPSGKAVKCG-GDITFDNNHTILFKQDYCEENGGAIST 174
QY 174 KTLSLTGTTMSALFSENSTSS---KKGAIQTSDALITIGNQGEVFSFSDNTSSDSGGAIFT 230
Db 175 KNLSLKNTGSISEFGNKSATGKGGAI CATGTVDTTNTATPLFSNNTAEEAGGAINS 234
QY 231 EASVTIENNAKVPIDNKVTTGASSSTTGDMSGGAICAYKSTSTDKVTLTGQMLLSNNT 290
Db 235 TGNCTITGNTSLFSENSVT---ATAG--NGGAL-----SGDADVTISGNQSVTFSGNQ 283
QY 291 STTAGGAIYVKKLELAS--GGTLTFLSNSVNGGTAPKGGAIADSDGELSADSGDIVF 348
Db 284 AVANGGAIYAKKUTLASGGGGGSIFFSNIVQGTAGNGGAISILAAGECSLSAEAGDITF 343
QY 349 LGNTVTISTTP-GTNRSSIDLGTSAKMTALRSAGRAIYFYDPIITGSSITTVTDVLKNET 407
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Qy 470 DSRLNDVGTLLPDAATSTIN--NLVINSSIDGAKKAKIETKATSKNUTLSGTTILLDP 527
Db 468 GSTLLMQPGTKL ADTEAISTKLKVVDLSALEGNKSVSIEAGANKTITLTSPVQDS 526
Qy 528 TGFYENHSLRNPSQSDILLELKAS-----GTVTSTAVIDPMGEKPFHYGYOGTWG 578
Db 527 SGNFYESHTINOAFQTPLVVFTAAATAASDIYDALLTSVPQTPEP-----HYVGQHWE 580
Qy 579 PIWVGCASTAPFNWKTCGYDNPRIOSGLVPNSLWNNAFIDISSLHYMETANEGLQSD 638
Db 581 ATWADTSTAKSGMTWTWTCYNPNERRASVVPDSLWSAFTDRTIQQLTMTSQANSIYQQ 640
Qy 639 RAWFCAGLSNFRHKDKTRGRPHISGGVYIGSNLHTCSDKILSAACQLRGDRDYFV 698
Db 641 RGLWASTANFFRHKDSGTNOAFRHKSYYGIYVGSAAEDFSENIFSVAFLFKGKDLEFI 700
Qy 699 AKNQGVYGTLYYOHNETYISLPCKLRPC--SLSYVPTTEIPVLFSGNLSYTHTDNDLKT 756
Db 701 VENTSHNYLASLYLOHRAFLGGLP--MPSFGSITDMLKDIPLILNAQLSYSYTKNDMDT 757
Qy 757 KYTTYTPVKSGMGNDFALPFGGRAICU-DESALFEQYMPFWKLFQVYAHQEGKEQGT 815
Db 758 RYTSYPAQSQTWNNGSALGLGSLALYLPKFAFPFGYFPFLKPQAVYSROONFKESGA 817
Qy 816 EAREFGSSRLVNALPIGIRFDKESCQDATNLTGYTVDLVRSPDCDTTLIRISGDSW 875
Db 818 EARAFDDGDLVNCISIPVIRLEKISEDEKNPFISLAYIGDVYRKPNRSRTSLMVSGASW 877
Qy 876 KTFGTNLAQAOLVLRAGNHCFNSFEARSQSFELRGSSRNVNVDLGAKYQF 928
Db 878 TSLCKNLARQAFASAGSHLTLSPHELVSEAAAYELRGAHYINVDCGLRYSF 930

RESULT 11
D72078
polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: D72078
R,Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72078
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-930 <ARN>
A:Cross-references: GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAD18590.1; PID:g437
A:Experimental source: strain CWL029
C:Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Query Match 40.6%; Score 1936; DB 2; Length 930;
Best Local Similarity 43.5%; Pred.No. 4.7e-97;
Matches 415; Conservative 165; Mismatches 325; Indels 48; Gaps 17;

Qy 1 MKSSFPRFVFSTFAIFPLSM-IAT---ETVLDSSASFQDNKNKNFNVRESQEDAGTYTLF 56
Db 1 MKIPLUKLLISSLTIVTBILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNVYL 60

Qy 57 KGNVTLENIPTGCTAITKSCFNNTKGDILTETGNGNSLLPQTUDAGTVAGAANNSSVVDKS 116
Db 61 SGNVIYI-NDACKGVALPGCCFTETGDLTFTGKYGFSFNTVDAGSNAGAAA-STTADKA 118

Qy 117 TTFTGFSLSFIAPSGSSIITTKGAVSCSTGSLSLTKNVSLSKPKNSTD--NGCAITA 173
Db 119 LTFTGPSNLSPAIAPAGTTVASGKSTLS-SAGALNLDTNGTILFSQNVSNEANNNGAITT 177

Qy 174 KTLSTGTGHWALSSENTSSKKGAIGTSDALTITGNQGEVSVSDNTSDDSAGAAITEAS 233
Db 178 KTLGISGNTSIIFTSNSAKKLGAIIYSSAAASISGNTGOLFVFMNNKGTCGCALGPAS 237

Qy	821	GSRLVNLALPIGIRFDKESDQDA--TYNLTGLGYTVDLVRSNPDCITTLRAIGDSWKTFG	879
Db	821	STGRLLNLSIPYGAKE--VGQDIGDSYTYDLSGFFVSDYVRNNPOSTATLVMSPDWKIRG	879
Qy	880	TNLAQALVLRAGNFCFNSPEAFQSFFELRGSSRNINVDLGAQYQF	928
Db	880	GNLSRQAFLLRGSNINYNVNSKELFGHYAMELRGSSRNINVDVGTKLRF	928

RESULT 14

F81591

polymorphic membrane protein G family CP0302 [imported] - Chlamydophila pneumoniae

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001

C:Accession: F81591

E:Read, T.D.; Bunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: F81591

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-949 <REA>

A:Cross-references: GB:AE002192; GB:AE002161; NID:G7189226; PIDN:AAF38159.1; P

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: CP0302

C:Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Query Match 38.9%; Score 1855; DB 2; Length 949;
Best Local Similarity 42.7%; Pred. No. 1.2e-92;
Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20

1 MKSSFPPKEVFSTFAIFP--LSMIATETVLDSSASEFDGN-KNGNESVRESOEADGCTTYIEK 57

22 MKTSTP BWVT VSSVT AFSCHLOS ANFEY I SDDDC ENVT DOCCMBDVT

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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

78 GDVFFIE-PGRGIFLSDSCFKQITIDNLTF LGNGHSLTFGFIDAGTHAGAAA-STTANKNL 135

118 TFIGPSSLSFIASPGSSITTGKGAVSCSTGSLSLTKNVSLFSKNFSTDNGGAI TAKTLS 177

136 TFSGFSLLSFDSSPSTVTGTGGLS-SAGGVNLENIRKLVVAGNFSTADGGAIKGASFL 194

178 LTGTTMSALFSENTSSKKGAIQTSDALITGNQGEVSFSDNTSSDSGAAIFTEASVTIS 237

195 LTGTSGDALFSNNSSSTKGGAIATTAGARIANNNTGYVRF,SNIASTSGGAIIDDEGTSIIS 254

238 NNABKVSEIDNNVWTCAGSSGTTCTNMCCCA TCGAYEATCCTTCTTATT TCACCAT CAA

[illegible]

CONFIDENTIAL
-----GORTONIMASSFEBTISNNALIFASNVAEISUGA 303

230 IIVATLEASGGULIFSRNSVNGGIAFKGATALEDSGELTSDSGDIVFLGNTVTST- 356

306 IHAKKLALSSGGFTFEFLRNNVSSAT - PKGGAISIDASGELSLSAETGNITFVRNLTITG 364

357 -TPGTRSSIDLGTSAKMTALRSAAGRAIFYDPIITGSSTTVDVLKVNETPADSALQY 415

365 STDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPIT--SEGTSSDVLKINNGSAGALNPY 422

416 TGNII FTGEKLSETEAADSKNLT SKLL OPVTI SGGTI SI KHGVYI LOTOA ETOO A DSRTEM 475

422 OCT 11 1964

2014 INDEPENDENT TOYOTA ACADEMY

[illegible]

483 DSGTILSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYES 542

535 HSLRNPQSYDILELKASGTVTS---TAVTPDPIMGEKFHYGYQGTWGPVWGTGASTT- 589

543 HMFSDQLFSLKITYDADVDTNVDISSLIPVPAEDPNSEYGFQGWV-VNWTDTATNT 601

QY 590 --ATFNTWKTYIPNPERIGSLVPSNLWNAFIDISSLHYMETANEGLQDRAPWCAGLS 647
 Db 602 KEATATWTKTGFVPSPERKSALVNCNTLWGVFTDIRSLQQLVEIGATGMEHQGFVSSMT 661
 QY 648 NFPHKDKSTKRRGRFRLHSGGYVIGNLTCSDKILSAAPCOLFGRDRDYFVAKNQGVYV 707
 Db 662 NFLHKTGDNKGRFRTSGGYVIGGSAHTPKDDLFTFAPCHLFARDKCFIAHNNRTY 721
 QY 708 GTLYYQHNET-----YISL-PCRLPCSLSYVTEIPVLFSGNLSYTHTDNLKTYTY 761
 Db 722 GTLFFXKSHSTLQPNVYLRGLGRKFSESAIEKFPREIPLALDVQVSPSHSDNRMETHYTS 781
 QY 762 PTYKSGWGNDSFALEFCGRAPICL-DESALFEQYMPMKLFQVYAHQEGFKEQGTAREF 820
 Db 782 PESEGSNSNECIAGGIGLDLPVLSNPHPLFKTFIPQMKVEMYVVSQNSFFESSDGRGF 841
 QY 821 GSSRLVNLALPIGIRFKESDCODA-TYNLTGLVTVLVRSDPCTTTLRISGDSWKTGF 879
 Db 842 SIGRLNLSIFVGAKEF-VQGDIGDSYTYDLSGFFVSDVYRNFPQSTATLWSPDSWKIR 900
 QY 880 TNLARQALVLRAGNHCFFNFAFQSFELRGSSRNYNVDLGAKYQF 928
 Db 901 GNLSRQAFLLRGSSNYVYNSNCELFCHYAMELRGSSRNYNVDVGTKLRF 949

RESULT 15
 E72130
 C:polymorphic membrane protein G family CP0761 [imported] - Chlamydia pneumoniae (stra
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
 C:Accession: E72130; G81541
 R:Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: E72130
 A:Molecule type: DNA
 A:Residues: 1-841 <ARN>
 A:Cross-references: GB:AE001586; GB:AE001363; MID:94376263; PIDN:AA18172.1; PID:9437627
 A:Experimental source: strain CWL029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: G81541
 A:Molecule type: DNA
 A:Residues: 1-841 <REA>
 A:Cross-references: GB:AE002235; GB:AE002161; MID:g7189672; PIDN:AAF38561.1; PID:g718967
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: pmp2; CP0761
 C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 32.9%; Score 1573; DB 2; Length 841;
 Best Local Similarity 39.4%; Pred.No. 1.8e-77;
 Matches 371; Conservative 121; Mismatches 310; Indels 140; Gaps 20;

QY 12 TFAIFPLSMIATETVLDSSAFDG-NKNGNFSVRESQEDAGTTLFKGNVTLENIPGTGT 70
 Db 15 TLSMNLGAATTEELSGNSPDGTTSTTSFSSKTSATDGTNYVPKDSVVIENVPKGE 74
 QY 71 AITKSCFNN--TKGDLFTFGNLSLLPQTVDAGTGAAGVNSVVDKSTTFIGFSSLSFI 128
 Db 75 TQSTSCFKNDAAAGDLNFGGFSFTFSNIDATTASGAAGTSEAAKNTVTLSGFSALSFL 134
 QY 129 ASFGSSITTKGKAVSCSTGSLSTKNVSLFLSKNFSNDNGGAIKTAKTSLTGTTMSALFS 188
 Db 135 KSPASIVTNGLGAINVK-GNLSLLDNDKVLIQNFSTGGGAINC----- 178
 QY 189 ENTSSKKGKAIQTSALITITNGQGVFSFSDNTSSDGAIFTTEASVTISNNAKVSIIDNK 248

Db 179 -----AGSLKIANNKSLSPFI--- 193
 QY 249 VTGASSSTTGDMSGGAICAYKSTDTKVTLTGNQMLLFNSNNTSTTAGGAIYVKKLELASG 308
 Db 194 -----GNSSSTGGAIHTKNTLTLSSG 214
 QY 309 GLTLFERNVNGGTAP-----KGAIAIEDSGELSLADSGLDIVFLGNVTSTTPTGT-NRS 363
 Db 215 GETLF-----QGNTPATAAGKGAIAIADSGTSLISGSDGDIIFEGNTIGAT--GTVSHS 267
 QY 364 SIDLGTSAKWTALRSAGRAIFYDPIITGSSSTTVTDVLKVNETPADSALQYTGNTIIFTG 423
 Db 268 AIDLGTSAKITARAAGHTIIFYDPIITGTSVADALNINSPTDGDKNKEYTGTIVFSG 327
 QY 424 EKLSETEAADSKNLSKLPVTLGGTSLSKHGVTLQTAFTQAQADSLEMDVGTTLRP 483
 Db 328 EKLTEAEAKDEKNTSKLLQNVAFKNGTVVLKGVDSVLSANGFSQDANSKILMDLGTSL-V 386
 QY 484 ADTSTI--NNIVINISSIDGAKAKIETKATSKNLTSLGTITLLDPTGTFYFNHSLRNQ 541
 Db 387 ANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVLAISDESFYQNGFLNEIH 446
 QY 542 SYD-ILELKASGTVTSTAVTPDPIIMGEKPHYGVQGTWGPVIMGTGASTTATENTWTKGYI 600
 Db 447 SYDGLLELDAGKDIVISADRS-IDAVQSPYGYQGN-TINWSTD-DKATVSWAKQSPN 503
 QY 601 PNPERIGSLVPSNLWNAFIDISSLHYMETANEGLQDRAPWCAGLSNFPFKDKSTKTRRG 660
 Db 504 PTAEQEAFLVPNLLMGSTFIDVRSFQNFIELGTGAPYEKRFVWAGISNVLHRSRENQK 563
 QY 661 FRHLGGYVIGNLTCSDKILSAAPCOLFGRDRDYFVAKNQGVYGGTLYYQHNETYIS 720
 Db 564 FRHSGGAVVGASTRMPGGDTLSLGAQLFARDKDYFMNTNFAKTYAGSLRLQHDASLYS 623
 QY 721 LFC-----KLRPCSLSYVTEIPVLFSGNLSYTHTDNLKTKY-----TTVPTVKSGW 769
 Db 624 VVSILLGEGGLEILLPVYVKTLPCSFYQLSYGHYTHDMKTESLPPTTSLDHTSWG 683
 QY 770 NDSFALFEGGRAPICLDESA---LFEQYMPMKLFQVYAHQEGFKEQGTAREFGSSRLV 826
 Db 684 GYVMAGELGTR--VAVENTSGRGFFQYETFPVKVQAVYARQDSFVELGAI SRDSDSHLY 741
 QY 827 NLALPIGIFPDKESDCODATNLTGTYVDLVRSPDCTTTLRISGDSWKTGTGNLARO 886
 Db 742 NLALPIGLIKLEKR--FAEQYHVAVMYSFVCRSNPKCTTTLLSNQGSWKTGSLARO 799
 QY 887 LVLRAGNHFCEFSNFEAFSQSFELRGSSRNYNVDLGAKYQF 928
 Db 800 GIVQASGFPSLGAALFNGFGEWGRSSRNVDAGSKIKF 841

Search completed: December 16, 2003, 10:54:43
 Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2003, 10:34:04 ; Search time 17 Seconds

(without alignments)
2567.105 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFPKFFVSTAIPLSM.....FELRGSSRYNVDLGAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2058	43.1	928	1 PM10_CHLPN	Q9rb65 chlamydia p
2	1982	41.5	928	1 PMP9_CHLPN	Q9z398 chlamydia p
3	1964	41.1	936	1 PMP7_CHLPN	Q9z898 chlamydia p
4	1936	40.6	930	1 PMP8_CHLPN	Q9z393 chlamydia p
5	1855	38.9	928	1 PM11_CHLPN	Q86164 chlamydia p
6	1573	32.9	841	1 PMP2_CHLPN	Q9z3a1 chlamydia p
7	1444	30.2	1276	1 PMP6_CHLPN	Q9z899 chlamydia p
8	1442.5	30.2	922	1 PMP13_CHLPN	Q9z295 chlamydia p
9	1377.5	28.9	973	1 PMP3_CHLPN	Q9z896 chlamydia p
10	1120.5	23.5	1013	1 PMPG_CHLTR	Q84879 chlamydia t
11	1051	22.0	987	1 PMPG_CHLMU	Q9pl45 chlamydia m
12	911	19.1	867	1 PMPI_CHLMU	Q9pl41 chlamydia m
13	863	18.1	878	1 PMPI_CHLTR	Q84882 chlamydia t
14	685.5	14.4	1609	1 PM21_CHLPN	Q9z6u5 chlamydia p
15	667.5	14.0	978	1 PM14_CHLPN	Q9z895 chlamydia p
16	666	14.0	947	1 PM19_CHLPN	Q9z813 chlamydia p
17	666	14.0	1723	1 PM20_CHLPN	Q9z812 chlamydia p
18	665.5	13.9	946	1 PM18_CHLPN	Q9z880 chlamydia p
19	647	13.6	952	1 PM16_CHLPN	Q9z882 chlamydia p
20	603.5	12.6	938	1 PM15_CHLPN	Q9z883 chlamydia p
21	603	12.6	975	1 PMPA_CHLTR	Q84417 chlamydia t
22	597	12.5	1016	1 PMPH_CHLTR	Q84880 chlamydia t
23	594	12.4	980	1 PMPH_CHLMU	Q9pl44 chlamydia m
24	587.5	12.3	976	1 PMPA_CHLMU	Q9pjy3 chlamydia m
25	576.5	12.1	1531	1 PMPD_CHLTR	Q84818 chlamydia t
26	559	11.7	1754	1 PMPB_CHLTR	Q84418 chlamydia t
27	549	11.5	976	1 PMPE_CHLMU	Q9pl47 chlamydia m
28	548.5	11.5	1672	1 PMPE_CHLMU	Q9pjy2 chlamydia m
29	544	11.4	1520	1 PMPD_CHLMU	Q9plb0 chlamydia m
30	541.5	11.3	964	1 PMPE_CHLTR	Q84877 chlamydia m
31	533.5	11.2	1460	1 PMPC_CHLMU	Q9pjy1 chlamydia m
32	523	11.0	1770	1 PMPC_CHLTR	Q84419 chlamydia t
33	490	10.3	1034	1 PMPF_CHLTR	P38008 chlamydia t

34 475.5 10.0 514 1 PM12_CHLPN Q9z3d6 chlamydia p
35 453 9.5 1025 1 PMPF_CHLMU Q9pl46 chlamydia m
36 269 5.6 2249 1 OMPA_RICRI P15921 rickettsia
37 251 5.3 2021 1 OMPA_RICCN Q52657 rickettsia
38 238.5 5.0 1025 1 SLAP_CAUCR P35828 saccharomyc
39 237.5 5.0 881 1 PRY3_YEAST P47033 saccharomyc
40 234 4.9 1645 1 OMPB_RICTY P96989 r outer mem
41 232 4.9 1643 1 OMPB_RICPR Q53020 r outer mem
42 230 4.8 995 1 YIQ9_YEAST P4442 saccharomyc
43 230 4.8 1250 1 YFAL_ECOLI P45508 escherichia
44 226.5 4.7 1609 1 FIG2_YEAST P25653 saccharomyc
45 224.5 4.7 2003 1 YDBA_ECOLI P33666 escherichia

ALIGNMENTS

RESULT 1

PM10_CHLPN STANDARD; Q9RB64; PRT; 928 AA.
AC Q9RB65; Q86163; Q9RB64; Q9S6P2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp10 precursor (Polymorphic membrane protein 10) (Outer membrane protein 5).
DE PMP10 OR OMP5 OR CP0303.
GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiales.
OC NCBI_TaxID=83558;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Dodson R., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE OF 1-914 FROM N.A.
RC STRAIN=CML029/VR-1310;
RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae.";
RL Infect. Immun. 67:375-383(1999).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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EMBL; AJ13034; CAB37071.1; -
 EMBL; AE002192; AAF38160.1; -
 EMBL; AP002546; BAA98657.1; -
 EMBL; AJ001311; CAA04671.1; -
 PIR; G81591; G81591.
 PIR; G86546; G86546.
 PHCI-2DPAGE; O86163; -
 TIGR; CP0303; -
 InterPro; IPR006315; Autotransport.
 InterPro; IPR003368; Chlamydia_PMP.
 Pfam; PF02415; DUF145; 2.
 TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 TIGRFAMs; TIGR01376; POMP repeat; 6.
 Outer membrane; Signal; Multigene family.
 SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 928 PROBABLE OUTER MEMBRANE PROTEIN PMP10.
 SQ SEQUENCE 928 AA; 97229 MW; 0590D5206A1DD0E1 CRC64;

Query Match 43.1%; Score 2058; DB 1; Length 928;
 Best Local Similarity 46.7%; Pred. No. 1,2e-104;
 Matches 444; Conservative 144; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSFPKVF-STFAIF---PLSMIATETVLDSASPDGNKN-GNFSVRESQDAGTYL 55
 Db 1 MKSQFWLUSLTLACTSCSTVPAVAENIGSDFDGTNTGTTPKNT--TTGDIYT 58
 QY 56 FKNVTLENIPGTGTAITKSCFNNTKGLTFTGNGSLLFQTVDAAGVAGAAVNSSVDK 115
 Db 59 LTGDITLQNL-GPSAALTGCFSDTTLSLFAAGYLSLFLNKS-SAEGAAL-SVTYDK 115
 QY 116 STTFIFGSSUSFIASPGSSITT--GKAVSCSTGSLTKVNLVSKNFSKFTDNGGAI 173
 Db 116 NLSLTGFSSTLTLAAPSSTVITPSGKAVKCG-GDLTFDNNGTILFKQDYCEENGGAIST 174
 QY 174 KTLSLGTTMSALFSENTSS--KKGAIQTSALATTGNGEVSFSDNTSSDGAIFT 230
 Db 175 KNLKKNSTGSISEFGNKSATGKGAICATGTVDTNNATPLFSNNIAEAGGAINS 234
 QY 231 EASVTISNNAKVFIDNKVTGASSSTTGMDSGGAICAYKTSITDKVTLTGNOMLFSNNT 290
 Db 235 TGNCTITGNTSLVSENSVI---ATAG--NGGAL-----SGDADVTISGNQSVTSGNQ 283
 QY 291 STTAGGAIYKKLELAS--GGLTLPNSVNGTAPKGAIAIEDSGELSLSDSDIVP 348
 Db 284 AVANGGAIYAKLTLASGGGGISFNNIVQGTAGNGGAISILAAEGCSLSAEAGDITF 343
 QY 349 LGNTVSTTP-GNRRSIDLGTSAKMTALRSAGRAIFYDPIITGSSITVTDLVKNET 407
 Db 344 NGNAIVATTPQTKRNSIDIGSTAKITNLRAISGHSIFFYDPIATANTADSTPLNKA 403
 QY 408 PADSALQYTGNIIFTGKLESEAAASKNLTSKLLQPVTLSSGGLSLKHKGVITQTQAF 467
 Db 404 DAGNSTDYSGSIVFSGEKLSEDAKVADNLITSLKQPVTLTGNLVLRGVILDTKGFTQ 463
 QY 468 QADSRLEMDVGTLEPA-DTSTINNLVINISSIDGAKKAKIETPKATSKNLTSLGTTLLD 526
 Db 464 TAGSSVIMDAGTTLKASTEEVITGLSIPVDSLGEKGVVIAAASAKNVALSGPILLD 523
 QY 527 PTGTFENHSLRPQSDVILELKASGTVTSTATVPDPIGKEKHYGQGTGVIW---- 582
 Db 524 NQGNVENDHDLGKTQDFSVQLSALGTATTIDVPATVPATPHYGQGTGWTG-MTWVDDT 582
 QY 583 -GTGASTATFNNTKGTGYPNPRIGSLVPSNLWNAFIDISLHLYMETANEGLQGDRAF 641
 Db 583 ASPTKTKATLNTNGYLPNPRQGPLVNSLWGSFSDIOAIQGVIERSLTLCSDRGF 642

QY 642 WCAGLSNFFHKDSTKTRGRHLSGGYVIGGNLHTCSDKILSAAFCQLFRDRDYFAKN 701
 Db 643 WAAGVANFLDKDKGKRYRKHSGGYAIGGAQTCSNLISFAFCQLFGSKDFLVAKN 702
 QY 702 QGTVYGTLYYQHNEYIYISLCKLRPCSLSYVP---TEIPVLFSGNLSVTHDNDLTKY 758
 Db 703 HTDYTAGAFYIQH---ITECSGFIGCLLDKLPFGSMHKEPLVLEGQLAYSHVSNLTKY 758
 QY 759 TTYPTVKGSGWGNDSFALFEGGRAPICLDESALFEQYMPFKLOFYVAHQEGKEQGTAR 818
 Db 759 TAYPEVKGSGWGNNAFNMMLGASHSPYVYLHCFDITYAPIKLNLTVIRODSFSEKGTGR 818
 QY 819 EFGSSSLVNLALPIGIRFKDESQDQATYNLTLGYTVDLVRNPDCTTTLRISGGSWKTF 878
 Db 819 SFDDSNLNLSLPIGVKPEKFSDCNDVSLVSYVPDLIRNDPKCTTALVLSGASWEY 878
 QY 879 GTNLRQALVLRAGNHCFNSNFEAFSPQSFELRGSSRNYNVDLGAQYQF 928
 Db 879 ANNLRQALQVRAGSHVAFSPMFVLGQFVFEVRGSSRYINVDLGGKQF 928
 RESULT 2
 PMP9_CHLPN STANDARD; PRT; 928 AA.
 ID PMP9_CHLPN AC Q92398;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable outer membrane protein pmp9 precursor (Polymorphic membrane
 protein 9) (Outer membrane protein 10).
 GN PMP9 OR OMP10 OR CPN0447 OR CP0306.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 Madesen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 role in immunopathogenicity.";
 RL Am. Heart J. 138:S491-S495(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=9920606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
 Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)

RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shiba T., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC
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 CC
 DR EMBL; AJ001311; CRA04672.1; -
 DR EMBL; AJ133034; CAB37072.1; -
 DR EMBL; AE001628; AAF18593.1; -
 DR EMBL; AE002192; AAF38159.1; ALT_INIT.
 DR EMBL; AP002546; BAA98658.1; -
 DR EMBL; D72077; D72077.
 DR EMBL; H86546; H86546.
 DR PHCI-2DPAGE; O86164; -
 DR TIGR; CP0302; -
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145.2.
 DR TIGRPFAM; TIGR01376; POMP_repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 928 PROBABLE OUTER MEMBRANE PROTEIN PMP11.
 SQ SEQUENCE 928 AA; 98903 MW; 788BCDD62C911402 CRC64;

Query Match 38.9%; Score 1855; DB 1; Length 928;
 Best Local Similarity 42.7%; Pred. No. 1.3e-93;
 Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;
 QY 1 MKSFPKFFVSTPAIFP--LSMTATETVLDDSSASPDGN-KNGNFSVRESQEDAGTTLPLK 57
 DB 1 MKTISFWLVSSVLAISCHLQSLANEELSPDSDFNIGNIDSGTFFPTKTS-----ATTYSLT 56
 QY 58 GNVLTENIFGTGTAITKSCFNNTKGDITFTNGNSLLFTQVDAGTVAGAAVNSVVDKST 117
 DB 57 GDVFFVE-FKGTPPLSDSCFKQTNDLTLFLNGHSLTFGFDAGTHAGAAA-STTANKNL 114
 QY 118 TFIGFSSLSFIAPSGSITTKGAVSCSTGSLTKRNVSLFKNFSTONGGAITAKTILS 177
 DB 115 TFGSGLLSFDSPSPSTVTATGQTLT-SAGGVNLENIRKLVVAGNFSTADGGAIGKASFL 173

QY 178 LTGTTMSALPSENTSSKKGAIQTSALITITGQGEVFSFSDNTSSDGAIFTASVTIS 237
 DB 174 LTGTSGDALFSNNSSSTKGAIATAGARIANNNTGVVFLSNIASTSSGGAIDDEGTSILS 233
 QY 238 NNAKVSFIDNKVYTGASSSTTGDMSSGCAICAYKTSTDTKVLITGNQMLLSNNSTSTTAGGA 237
 DB 234 NKKFLYP-----EGNAKTT-----GGAICNTKASGSPFLIINNKTLLIFASNAVETSGGA 284
 QY 298 IYVKLELASGGTLTFSRNSVNGGTAPKGAIAIEDSGELSLSDSGSDIVFLGNTVTST- 356
 DB 285 IHAKLALSSGGTFEFLRNNVSSAT-PKGALSIDASGELSLSAETGNTITFRNTLITTTG 343
 QY 357 -TPGWRSSIDLGTSAKMTALSAAGRAIYFVDPIITGSGSTTVTDVLKVNTPADSALOY 415
 DB 344 STDTPKRNAINIGNSGKFTELRAAKNHTIFFYDPIT--SEGTSSDVLKINNGSAGALNEF 401
 QY 416 TGNIIPTGKLSATEAADSKNLTSLKLOPVTLSSGGTSLSKHGVTLCOTQFTQOASRLEM 475
 DB 402 QGTILFSGETLTADLKVADNLKSSFTQPVLSGGKLLQKGVTLLESTFSQOBSAGLLGM 461
 QY 476 DVGTTLE-PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTILLDPTGTFYEN 534
 DB 462 DSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLANLIDIEGNIYS 521
 QY 535 HSLRNPOSVDILELKASGTVTS-----TAVTPDPINGEKHYGYQGTWGPVWGTGASTT- 589
 DB 522 HMFSDHQLFSLKITTVDADVDTNVDISSLIPVPAEDPENSEYGFQGWNV-VNMTTDTATNT 580
 QY 590 --ATFNWTKTGYIPNPERIGSLVPSNLWNAFIDISLHVLMTANEGLOGDRAFWCAGLS 647
 DB 581 KEATATWTKGVFSPERKSAVLCNTLWGVFTDIRLQOLVEIGATGMEHKGQFWSSMT 640
 QY 648 NFFHKDSTKRRGFRHLGGYVIGNLHTCSDKILSAAPCOLFGRRDRDYFVAKNQGVYV 707
 DB 641 NFLHKTGDNRRKGRHTSGYVIGSAHTPKDDLTFACHLFARDKOCFIAHNSRTYV 700
 QY 708 GTLYYQHNET-----YISI-PCKLRPCSLSYVTPPIVPLFSGNLSYTHTDNDLTKYTTY 761
 DB 701 GTLFFKHSHTLQPNYLRGLGRAKFAIEKEFRIEPLALDVQVSFSHSDNRMETHYTSL 760
 QY 762 PTVKSGWGNDSFALEFFGGRAPICL-DESALPEQYMPMKLQFVVAHQEGFKQGTREARF 820
 DB 761 PESEGSWSNECIAGGIGLDLPVLNPNPLFKTIFIPQMKVEMVYVSQNSFFSSSDGRGF 820
 QY 821 GSSRLVNALPIGIRFDKESDQDA-TYNLTILGYTDLVRSNPDCTTLTIRISGDSWKTFG 879
 DB 821 SIGRLNLISIPVGAKF-VQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLWMSPDWKLKG 879
 QY 880 TNLARQALVLRAGNHFCNSNFEARSPFSFELRGSSRNYNVDLGAQYQF 928
 DB 880 GNLSRQAFLLRGSNNYVNSNCELFGHYAMELRGSSRNYNVDVGTKLRF 928
 RESULT 6
 ID PMP2_CHLPN STANDARD; PRT; 841 AA.
 AC Q9Z3A1; Q9RB73;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable outer membrane protein pmp2 precursor (Polymorphic membrane
 DE protein 2) (Outer membrane protein pmp2 precursor (Polymorphic membrane
 DE PMP2 OR OMP7 OR CPN0013 OR CP0761).
 GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugeard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their

Db 1183 LTFKHESAKPPSALLTLTGVAVDAYDRHDPHCITSL-TNGTWSFTATNLSRQAFPAESG 1241

Qy 894 HFCNSNFARSQSFELRGSRNNVNLGAKYQF 928

Db 1242 HLKLLHGLDCFASGSCELSSRSRSTNACGTRYSF 1276

RESULT 8

PMPL CHLPN STANDARD; PRT; 922 AA.

ID QP29G5; Q9K1Y9; Q9Z4H9;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable outer membrane protein pmpl precursor (Polymorphic membrane protein 1) (Outer membrane protein pmpl precursor (Polymorphic membrane protein 1) OR OMP6 OR CPN005 OR CP0770).

GN Chlamydia pneumoniae (Chlamydia pneumoniae).

OS Chlamydia pneumoniae (Chlamydia pneumoniae).

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83558;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VR1310;

RA Christian G., Boesen T., Hjerno K., Dagaard L., Mygind P., Madsen A.S., Knudsen K., Falk E., Birkelund S.; "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity"; Am. Heart J. 138:S491-S495(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CW1029;

RA MEDLINE=20007584; PubMed=10539856;

RA Kalmann S., Mitchell W., Marathe R., Lammell C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=AR39;

RA MEDLINE=92206606; PubMed=10192388;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=J138;

RA MEDLINE=20330349; PubMed=10871362;

RA Shirai M., Hirakawa H., Kinoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CW1029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).

CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

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DR EMBL; AJ133035; CAB37075.1; -

DR EMBL; AE001585; AAD18163.1; -

DR EMBL; AE002237; AAF38570.1; -

DR EMBL; AP002545; BAA98215.1; -

DR PIR; B72131; B72131.

DR PIR; B86491; B86491.

DR TIGR; CP0770; -

DR InterPro; IPR003368; Chlamydia_PMP.

DR Pfam; PF02415; DUF145; 1.

DR TIGRFAMs; TIGR01376; POMP repeat; 5.

KW Outer membrane; Signal; Multigene family; Complete proteome.

FT SIGNAL 1 26 POTENTIAL.

FT CHAIN 27 922 PROBABLE OUTER MEMBRANE PROTEIN PMP1.

FT CONFLICT 14 14 F -> L (IN REF. 1).

FT CONFLICT 375 375 Y -> C (IN REF. 1).

FT CONFLICT 606 606 D -> N (IN REF. 1).

SQ SEQUENCE 922 AA; DFF2ABG333AB031C CRC64;

Query Match 30.2%; Score 1442.5; DB 1; Length 922;

Best Local Similarity 36.9%; Pred. No. 3.6e-71;

Matches 351; Conservative 156; Mismatches 381; Indels 63; Gaps 26;

Qy 5 FP-KFVSTFAIFPLSMIAIETVLDSASPCNGKNGNFSVRESQEDAGTTVLFKGNVTLE 63

Db 8 FPLVFSFTLLSVPTLSAATISLTPDSFPGDSQN--AERSYVNVQAGDVYSLTGDVVIS 65

Qy 64 NIPGTGTAITKSCFNNTKGLDTFTGNGNSLLFQTVDACTVAGAAVNSVVDKSTT-PIGF 122

Db 66 NV--DNSALNKACFNVTSGSVTFAGNHGGLYFNINISGTYKEGAVLCCQDPQATARSGF 123

Qy 123 SLSFIASPGSSITTKGAVSC--STGSLSLTKNVLFSKXNFTDNGGAIKATLSLTG 180

Db 124 STLSFIQSPGDIKEQG-----CLYSKVALMLNNVVRFEQNKQSKTGKGAISGANVTIVG 178

Qy 181 TTMSALPSENTSKKGAIQTSALTITGNGEVSFSDNTSSD--SGAAIFTEASVTTNN 239

Db 179 NYDSVSPYQNAAT-FGGAIHSSGFLQAVNQAEIRFPAQNTAKNGSGGALYSDGIDIDQN 237

Qy 240 AKVSFIDNKVTGASSSTTGDMSGCAICAYKTSTDTK---VTLGNQMLFSNNTSITAG 295

Db 238 AYVLFRENE-----ALTATGKGAGVCCLTSGSGSTPVPIVTFSDNQVFERHNSINGG 292

Qy 296 GAIYVKLELASGGITLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDVFVLTGNTVTS 355

Db 293 GAIYARKLISISSGGPTLFINNISYANQNGLGAITDGTGEISLSAEGKITTFQGN--RT 350

Qy 356 TTPGTNRSIDLGSNAKTAALRSAGRAIYFDYDITGSSSTTVTDVLKVNTPADSAQY 415

Db 351 SLPLFN--GIHLLQNAKFLKLAENGYSIEFYDIT--SEADGSTQLNININGDPKNK--EY 404

Qy 416 TGNITFTGEKLSATEAADSCKLTKLPVTLGGTSLSKHGVTLLQTAQFQQADSRLEM 475

Db 405 TGTILFSGEK---SLANDPRDFKSTIPQNVNLSAGYLVIKEGAETVSKFTQSPGSHLV 461

Qy 476 DVGTTL-EPADTSTNNLVINISSIDGAKKAK-IETKATSKNLTLSGTITLLDPTGTFYE 533

Db 462 DLGKTLIAKEDIATGLAIDIDSLSSSTAIVKANTANKQISVTDSEIISITGNAYE 521

Qy 534 NLSLNQSYDILELK--ASGTVTSTA-----VTPDPIMGEKHYGYQGTWGPVW-GTG 585

Db 522 DLRRNSQTFFLLSLFEGAGGSVTVTAGDFLPVSP-----HYGQGNW-KLAWTGTG 572

Qy 586 ASTTATFNWTKGYIPNPERIGSLVPNSLWNAFTDISSLHVLMTANEGLOGDRAPWCAG 645

Db 573 -NKVGEFFWKINKYPRPEKEGNLVPNLLMGNADVRLMQVQVTHASSQTDRGLWIDG 631

Qy 646 LSNFPHKDSKTRGRPHLSGGYVIGGNLHTCSDKILSAAPQLFGDRDRYFVAKNQGTV 705

Db 632 IGNEFFHVSASEDNIRYHNSGGYVLSYNNETPKHYTSMASFQSLFSKDKYAVNSNFRM 691

Qy 706 YGGTLYTQHNET-----YISLPCKLRPCSLSYVETIP-VLFSGNLSYTHTDNDLKTKY 758

Db 692 YLGSYLYQYTTSLGNLIFRYASRNPNNVNGILSRRLQNLPLMIFHFLCAYGHATNDKTDY 751

Qy 759 TTYPTKSGWGNDSFALEFGGRAPICLDESA-LFEQYMPMKLOFVYAHOBGFKEQGTGA 817

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Db 752 ANFPWKNWRNNWCATECGSMPLLVFENGRLFOGAIPEMKLQVLVAYQGFKEATTADG 811
QY 818 REFGSSFLNALPIGIRPKESDCQADATNLTGTVDLVRNPDCITTLIRISGSWKT 877
Db 812 RRSNGSLTISVPLGRFRFKLALSQVLYDFSFYIPDFRKPDSCEAAALVSGDSWL 871
QY 878 FGTNLQALVLGRAGNHFCNSFPAFSQSFELRGSSRNYNVDLGAQYOF 928
Db 872 PAAHVSFAVGSCTGYRHENDYTELLCRGSIIECRPHARNYINCSKFRF 922

RESULT 9
PM13 CHLPN
ID PM13 CHLPN STANDARD; PRT; 973 AA.
AC Q92896; O9K2A1; Q92410;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp13 precursor (polymorphic membrane
protein 13) (outer membrane protein 14).
GN PMP13 OR OMP14 OR CPN0453 OR CP0299.
OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marache R., Lammel C., Fan J., Hyman R.W.,
OLingher L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
SEQUENCE OF 1-262 FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Wgind P.,
Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
(POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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CC -----
DR ENBL; AB001629; AAD18595.1; -
DR ENBL; AB002191; AAF38156.1; ALT_INIT.
DR ENBL; AP002546; BAA98660.1; -
DR ENBL; AJ133034; CAB37074.1; -
DR PIR; B86547; B86547.
DR PIR; F72076; F72076.
DR PHCI-2DPAGE; Q92896; -
DR TIGR; CP0299; -
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF03797; Autotransporter_1.
DR Pfam; PF02415; DUF145_3.
DR TIGRFAMs; TIGR01376; POMP repeat; 7.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 973 PROBABLE OUTER MEMBRANE PROTEIN PMP13.
FT CONFLICT 258 258 N -> Y (IN REF. 4).
SQ SEQUENCE 973 AA; 102761 MW; E02A69F611DEBFE2 CRC64;

Query Match 28.9%; Score 1377.5; DB 1; Length 973;
Best Local Similarity 34.8%; Pred. No. 1.3e-67;
Matches 350; Conservative 153; Mismatches 391; Indels 113; Gaps 25;

QY 1 MKSSPKKVFST-----FAIFPLSMIAETVLDSSASFGCNKNGNFSVRESQEDAGTVL 55
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 56
1 MKTIRKFLISTTLAPCFA---STAFTVEVIMPSENFDSGSGKIFPYTLLSDPRGTLCI
QY 56 FKGNTVLENIPTGTATKSCFNNTKGDLTFTFGNGLLFTQVDAGTVAGAAVNSVVDK 115
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 116
57 FSGDLVIANLDNAISRTSSCSFNAGALQILKGGVFSFLNI-RSSADGAIAISVITON 115
QY 116-----STTFPGSLSF-----IASPGSITTKGAVSCSTGSLSLTKNVLFSKFNFS 164
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 174
116 PELCPLSFSGFQMIFFDNCELSLTSASNVIPHASAIYATTPML-FTNNDILFOYKNS
QY 165 TDNGGAITAKTILSLGTTMSALFSENSSKKGATQTSDALITGNGVSVFSD----- 218
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 218
175 AGFGAIRTSTIETIKSLFNNGSISNGGALTGSAAILNINNSAPVIFSTNATGY 234
QY 219-----NTSSDSGGAIFTEASVTISNAKVSFIDNKVTCASS- 254
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 294
235 GGAIVLTGSGMLTSGNLGVLVFNSSRGGAIYANGVTFNNSDLITPONTASPNLSL
QY 255-----STTGDMG-GGAI-C---AYKSTDTKVLTKNQMLLFNSNTSTTAGGAIY 299
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 354
295 PAFTPTPTTPAVTPLLGYGGAIFCTPPATPPPTGVSITSGENSVTFLENIASEQGALY
QY 300 VKKLELAGGLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVPLGN-TVTSITP 358
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 358
355 GKKSIDSNKSTIFL-----GNTAGKGAIAIPESGELSLSANQGDILFNKNLSITSGTP 409
QY 359 GTNRSSIDLTSAKMTALRSAGRAIYFYDPIITG--SSTVTVDLVKN-ETPADSALQY 415
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 465
410 --TRNSIHFGDKAFATLGATGYLYFYDPIITSDDLASAASAAATVNVNPRASADGA-Y
QY 416 TGNIIPTGEKLSEREAASKNLTKLQPVLTSGTSLSKHGVTILQTAFTQADSRLEM 475
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 525
466 SGTIVFSGETLTATEAATPANATSTLNQKLEGGTALRNGCATLVNHFNTQDEKSVVIM
QY 476 DVGTITLEPADTS-----TNNLVINISSIDGAKKAKIETKATSKNLTSGTITLLDPT 528
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 585
526 DAGTTLATNGANNVDGAILNKLVINDSLDGTAKAAVVNVQSTNGALTISGTLGVKNS
QY 529 GTFFENHSLRNP--QSYDILELKA-SGTVTSTAVTPDPIMGEKHYGQGTWGPVIMCTG 585
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 644
586 QDCDCHGKFNKDLQOVFIKATSNVTITDPSLGTNGYQQSPYGGQTFWEFTIDTT-
QY 586 ASTTATFNWTKTYIPNPERIGSLVPNSLWNAFIDISSHLVIMETANEGLOQDRAFWCAG 645
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 702
645 -THTVTGNWKKTYLPHERLAPLIPNSLWANVIDLRAVSQASAAADGEDVFG-KQLSITG
QY 646 LSNPFHKDSTKTRGRFHLSCGYVIGGNLHTCSDKILSAAFQCLFGRDRDYFVAKNQGTV 705

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Db 703 ITNFFHANHTGDARSYRHMGVLYINTYTRITPDAAALSLGFGQFTKSKDYLVGHGHSNV 762
QY 706 YGGLTYXQHNETYISLPCKLRPCSLSVVPEIPVLESGNLS---YHTDNDLTKYTYTP 762
Db 763 YFATVYVSNITKSLFG-----SSRFSGGTSTRTVYSRNEKVKTSYTKLP 806
QY 763 TVKSGMNDNFALFEGGRAPICLDESAL-PEQYMPFMKIQFYVAHQEGFKQGTAREBG 821
Db 807 KGRCSMNSNCWLEGNLPITLSSRLNLKQIIPVKAFAVATYHGGIOENTPEGRIFG 866
QY 822 SSRVNLALPIGRFKESQCDATYNTLIGYTVDLVRNPDCPTTLIRISGDSWTKFTGN 881
Db 867 HGHLNVAVPVGRFGKNSHNRPDFYIIIVAYAPDVYRHNPDCTTLPINGATWTSIGNN 926
QY 882 LARQALVLRAGNHFCFNSNEPASFQSFELRGSRRNRYNDLGAQYOF 928
Db 927 LTRSTLLVQASSHTSVNDVLEIFGHGCDIRRTSRQYTLIDIGSKLRF 973

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RESULT 10

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PMPG CHLTR
ID PMPG CHLTR STANDARD; PRT; 1013 AA.
AC O84879;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable outer membrane protein pmpG precursor (Polymorphic membrane
protein G).
DE PMPG OR CT871.
GN Chlamydia trachomatis.
OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759 (1998).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
(POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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CC EMBL; AE001360; AAC68469.1;
CC PIR; G71460; G71460.
CC PHCI-2DPAGE; O84879;
CC InterPro; IPR006315; Autotransport.
CC InterPro; IPR005546; Autotransporter.
CC InterPro; IPR003368; Chlamydia_PMP.
CC Pfam; PF03797; Autotransporter; 1.
CC Pfam; PF02415; DUF145; 1.
CC TIGRFAMs; TIGR01414; autotrans barl; 1.
CC TIGRFAMs; TIGR01376; POMP repeat; 6.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 1013 PROBABLE OUTER MEMBRANE PROTEIN PMPG.
SQ SEQUENCE 1013 AA; 107366 MW; F0927743COA651DD CRC64;

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Query Match 23.5%; Score 1120.5; DB 1; Length 1013;
 Best Local Similarity 29.6%; Pred. No. 1.4e-53;
 Matches 313; Conservative 160; Mismatches 409; Indels 177; Gaps 33;

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QY 1 MKSFFPKVFSTFAIFPLSMIA-----TETVLDSSASFDGNK-NGNFSVRESQBDAGTYYL 55
Db 1 MOTSFHKKFLLSMILAYSCCSLGGGYAAEIMIPQGIYDGETLTVSPYTVIGPDSGTTVF 60
QY 56 PKGNVTLENIPGTGTAITKCPNNTKGDLLFTPTGNSNLLPQTVDAGTVAGAAVNSVVDK 115
Db 61 SAGELTLTKNDNSIAALPLSCFGLNLLGSFTVLGRGHSLTFENIRTS-NGAALSDSANGS 119
QY 116 STTRIFGSSLSF-----IAGPGSSITTKGAVSCSTGSLSTKNVSL 157
Db 120 LFTTIEGKELSFSCNCSLLAVLPAATNNGSQPTTSTPSNGTIYSKT-DLLLLNNEKF 178
QY 158 LFSNFTDONGGAIKTAKTSLTGTMTSALFSENSTSKKGAIQTSDAITITNGQVSP- 216
Db 179 SFYNLVSGDGGAIIDAKSLTVQGISKLCVPQENTAQADGACQVTVTSFSAANEAPIAFI 238
QY 217 -----SDNTSSDS-----GAAIFTEASVT 235
Db 239 ANVAGVRGGGIAVQDQGGQVSSSTSTEDPVVFSRNTAVEPDGNVARVGGGIYSYGNVA 298
QY 236 ISNNAKVSFIDN-----KVTGASSSTTGDG--SGGAI-C-----AYKSTDTTKVT 277
Db 299 FLNNGKTLFLNNVASPVVIAAEQPTNGQASNTSDNYGDGGAIFCKNGAQAGSNNSSVS 358
QY 278 LTGNQMLLFSNNTSTTAGGAIYVKLELASGLTLFSRNSVNGGTAPKGAIAIEDSGEL 337
Db 359 FDGEGVFFSNNVAAAGKGGAIYAKKLSVANGCPVQFLGNIA-----DGAIIYLGSEGL 413
QY 338 SLSADSGDIVPLGN---TVTSTTPTGN-----RSSIDLGTSAKMTALRSAGRAIFYDP 389
Db 414 SLSADYGDIIIFDGNLKRKTAKENAADVNGVTVSSQAIISMGSGGKITTLRAGAGHQLLPNDP 473
QY 390 ITTGSSTT-----VTDVLKVNTPADSALQYTGNIITFTEKLSSETAADSNNLSKLLQPV 445
Db 474 IEMANGNNQPAQSSEPLKINDGEG---YTGDIVFA-----NGNSTLYQNV 515
QY 446 TLSGGLSLKHGVTLQTAFTQQADSRLEMDVGTGLE-----PADTS--TINNVL 493
Db 516 TIEQGRIVIREKAKLSVNSLSQTGS-LYMEAGSTLDFVTFPPQPPQPPAANQLITLSNLH 574
QY 494 INISSI---DGA-----KKAKIETKATSKNLTLSGTTIPLDPTGTFYENHS-LR 538
Db 575 LSLSLLANNAVTPNPPTNPPADDSHPALIGSTTAGSVTISGPIFFDLDDTAYDRYDWLG 634
QY 539 NPQSDVILELKASCTVSTATVPDPMGEKF-HYGYOGTWGPIVWGTCGASTATF-----N 593
Db 635 SNQKIDVLKQL-GTQPSANAPSDLTGNEPMKYGYGGSW-KIAWDPTNANGPYTLKAT 692
QY 594 WTKTGYPNPERIGSLVPSNLWNAFIDITSLIHYMETANEGLOQDRAPWCAGLSNFFHKD 653
Db 693 WTKTGYNFGPERVASLVPSNLWGLSILDIRSAHSAIQASVDGRSYCRGLWVGVSNNFFVHD 752
QY 654 STKTRGRPHLSGGVVGNNLHTCSDKLSAFCQLFGRDRDPYVAKNQGTIVGTTYYQ 713
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QY 714 HNETYISLPCKLRPCSLSVVPEIPVLFSG---NLSYTHTDNDLTKYTYTPTVKGSWGN 770
Db 810 -----LSTQALCG-SY-----LFGDAFIRASYFGNQHWKTSYTTAEBSDVWRDN 854
QY 771 DSFALEFGGRAPICLDESALF-EQYMPFMKIQFYVAHQEGFKQGTAREFGSRLVNLA 829
Db 855 NCLVGEIGVGLPIVITTSKLYLNELRPFVQAEFSYADHESFTBEGDQARAFSRGHLNLS 914
QY 830 LPIGRFKESQCDQATYNTLIGYTVDLVRNPDCPTTLIRISGDSWTKFTGNLARQALVL 889
Db 915 VEVGVKFRCSSTHPNKYSFMGAYICDAYRTISGTQTLTLLSHQETWTTFDAPFLARHGVI 974
QY 890 RAGNHFCFNSNFEAFSQSFELRGSRRNRYNDLGAQYOF 928
Db 975 RGSWYASLTSLNIEVGHGRYRYRTSRGYGLSAGSKVRFP 1013

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RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linner K., Weidman J., Khouri B., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.,
 RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RT Nucleic Acids Res. 28:1397-1406(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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 CC EMBL; AE002294; AAF39136.1; -;
 DR PIR; F81721; F81721.
 DR TIGR; TC0267; -;
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145; 1.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 867 PROBABLE OUTER MEMBRANE PROTEIN PMPI.
 SQ SEQUENCE 867 AA; 95017 MW; 557994185A95652 CRC64;
 Query Match 19.1%; Score 911; DB 1; Length 867;
 Best Local Similarity 29.5%; Pred. No. 2.7e-42;
 Matches 281; Conservative 144; Mismatches 384; Indels 144; Gaps 30;
 QY 17 PLSMIATETVLDSSAFDGNKNG-----NFS---VRESQED-----AGTYILF 56
 DB 18 PTAIFGQDALOKSALITKPNPSIVCTFLEDCMTENFSPALLSHARQDDPLYIINTH-- 75
 QY 57 KGNVTLENT-PGGTGTATKSCFNNTKGDLTFTGNGSLLFQTVADTVAGAAVNSVVVDK 115
 DB 76 --NWFVSNLHPST-----NEERFLKEKGLSI-----Q 101
 QY 116 STTFIGFSSLSFTASPGSSITTKGAVSCSTGSLTKVNSLLPKNFSTNGAITAKT 175
 DB 102 DFRFLFTDCSSSTEDSPSILYHK-----NGQLFLRNNGNMFYRNHSEGGGALSTDA 155
 QY 176 LSLTGTMTSALFSENTSSKKGAIQTSDALTTGNQGEVFSFSDNTSSDSGAIFTEASVT 235
 DB 156 LFLQHYLYFTNFENSARKNGAIQ-AQTLSLRNVSSLSFRNRANLNGAICCNQLIC 214
 QY 236 ISNNAKVSPFDNKVTGASSSTTGDMSGGAICAYKTSITDTK---VLTIGNQMLLFNNSTST 292
 DB 215 SGNVNPLFFTTNSA-----LNGGAICCNQNEKGLSLAYNQETLFGNSAK 264
 QY 293 TAGAIVYKLELASGLTLFSPNSVNGGTAPKGGAIATEDSGELSLSDSGDVFELGNT 352
 DB 265 EKGGAITRHMVLRHNGPVSFVNS-----AKLGGAIATQSGGSUILLAGGGSVLFQNNIS 319
 QY 353 VTSTTPTGNRSIDLGTSAWTAALRSAGRAIYFYDPIITG-----SSTVTVDLVKNE 406
 DB 320 CHFSDQGTVENAILEKNALLSLEARHG-DILFFDPIQEVVSPFSTTSALTPLRI-Q 377
 QY 407 TPADSALOYTGNIFTGEKLESETAADSKNLTSLKLLQPVTLSGTSLKHGVTLQOAPT 466
 DB 378 TTNTRA-----VIFSSENLSKEKTEA-NLSKIQPIELQSGCIVLDRVILSAPSUS 430
 QY 467 QQADSRLEMDVGTTLLEPADTSTINNVINISSIDGAKAKIEFKATS-KNLTSGTITLL 525
 DB 431 QAFQALLVMDVGLTSSDLKTLISIPHSITDENSIVSIQSPTSIQIFLNS-----486
 QY 526 DPTGTFTFVNHSLRNPOSYDILELKASQTVTSTAVTPD-PIMGKFKHYGQGTWGPVWGT 584

Db 487 -EHENFVENVELLSKQDKDIPLL-----SLPKGLPHDPLDQGNLSSHFGYQGDWN-PSMQT 540
 QY 585 G-ASTTATFNWTKTYGIPNPERIGSLVPSNLWNAFIDISLHYLMETANEGLQGDRAF-- 641
 Db 541 SDQRETLVANWNTANSYIPHPERQSAULVANTLWNTYSDMQAVQSMINTTAQG--GAYLFT 598
 QY 642 WCAGLSNFF--HKDSTKTRGRFRHLSGGYVIGGNLHTCSDKILSAFCLQFGRDRDYFVA 699
 Db 599 WGSVAVSNLFLYSHGNSGKSTDNWKRSLGYLFGISTHSLDDHSCFLAAGQLFKSSDSFT 658
 QY 700 KNOGTIVGGTLYYQHNETYISLPCKLRPCSLSVVTEIP---VLPFGNLSYTHTDNLIK 756
 Db 659 SADTTSY-----IAAIQIATSLIKISAQACYNESITHELKT 695
 QY 757 KYTTYPTVK-GSWGNSDFALEFGGRAPICLDESALFEQYMPFMKLFQVVAHQEGKQGT 815
 Db 696 KYRSFKSKEGFAHWSVAVGEIGASIPVNSGSLFSSFSIFSKLQFGSGKQDGEESRG 755
 QY 816 EAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTGYTVDLVRSNPDCTTTLIRISGDSW 875
 Db 756 EARAFAADSSFTNISLPVGIAFEKKSKQTRNYVHFLGAYIQDLKRCVSGPVTLLKNSVTM 815
 QY 876 KTFGTNLARQALVLRAGNHCFNSNEAFSQSFELRGSSRNVDLGAQYOF 928
 Db 816 DAPMANLDSRAWNFRLTNQRAHLH-RFQTLVNSMYLGRGQSYSLDLGTTIYRF 867
 RESULT 13
 PMPI_CHLTR
 ID -PMPI_CHLTR STANDARD; PRT; 878 AA.
 AC 084882;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable outer membrane protein pmpi precursor (Polymorphic membrane
 DE protein 1).
 GN PMPI OR CT874.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UM-3/Cx;
 RX MEDLINE=9900809; PubMed=9784136;
 RA Stephens R.S., Kallan S., Lammel C.J., Fan J., Marache R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RA "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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 CC EMBL; AE001361; AAC68472.1; -;
 DR PIR; B71460; B71460.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; DUF145; 1.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 878 PROBABLE OUTER MEMBRANE PROTEIN PMPI.
 SQ SEQUENCE 878 AA; 95592 MW; DF1FIA31707EE48B CRC64;

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Query Match      18.1%; Score 863; DB 1; Length 878;
Best Local Similarity 30.1%; Pred. No. 1.1e-39;
Matches 260; Conservative 124; Mismatches 368; Indels 112; Gaps 23;

Qy 118 TFIGFSLSPFASPGSSITTKGAVS-----CST-----GSLSTTKN 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 SYCNFVSKLHITDPKEALFKKGLSLQNFRLSFTDCSSKSSPSIIHKNGQLSLRN 133

Qy 155 VSLLPKFNFTDNGGATATKLSLTGTMALSENSTSSKGAIGAIQTSDDLTITNGGEV 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 GMSFCFCAHAGGGAISADAFSLQHNLYLFTAFENSSKNGGAIGAIQTSFSLRN 192

Qy 215 SFSDNTSSDGAIFTEASVTISNAKVSFIDNKVTGASSSTTCDMSGGGAICA---YKTS 271
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 SFARNADINGGAICCSNLICSGNVNPLFTGNSAT-----NGGAICCSIDLNTS 242

Qy 272 TDKVTLTGOMLLFSNNSTTTAGGAIYVKKELASGGLTLFERNVNGGTAPKGAIAI 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 EKSLSLACNQETLFASSAKERKGAIAKHMVLRVNGPVSVFINNS-----AKIGGAIAI 297

Qy 332 EDGSELSSADSDGIVFLGNVTSTTPTNRESDIDLTSAKMTALRSAGRAIYFDPI 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 QSGSLSILAGESVLFQNNQSRTSQGLVNAIYLEKDAILSLSEARNG-DILFDP 356

Qy 392 TGSSTTVDVLKVNTPADSAALQVT-----GNIFTGEKLSLSEAA 432
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 QESSS-----KESPLPSLQASVTSPTPATAPLVIOTSANRSVFSSELSSEKT 408

Qy 433 DSKNLSKLLQPVTLGGTSLKHGVTLOQATQQAQSDRLMDVGTTLLEPADTSTINN 492
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 409 PD-NLTSQLOQPIELXSGRLVLDRAVLSAPLSQDPQALLIMEAGTSLKTSDDLK 467

Qy 493 VINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTCFVENHSLRNPSQYDILEK 552
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 SIPHLSDTEKSVTH-----APNLISQKIFLSNGDENFYENVNELLSKEQNNIPL 522

Qy 553 TVTSTAVTPDPIIMGEKFGHYQGTWGPVW---GTGASTTATFNWTKGTGYPNPERIG 609
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 523 KEQSHLHLPDGNLSS---HFQYQGDW-TFSWKDSDEGHSLIA---NWTPKYVHPER 577

Qy 610 VPSNLWAFDIDSLHYLMEANEGLOGDRAF--WCAGLSNFF--HKDSTKTRRGRPH 665
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 578 VANTLWNTYSDMQAVQSMINTIAHG--GAYLEGTWGSVAVSNLIFYAHDSSGKPID 635

Qy 666 GGVIIGNLHTCSDKILSAFACOLFGRRDRDYFAKNQGTQYGGTLYIYQHNETYIS 725
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 636 LGVFLGISTHSLDDHFCUAGQLLKGKSDSFITSTETSYIATVQAQ-----LAT 688

Qy 726 RPCSLSYVTEIPVLFSGNLSYTHTDNDLTKYTYPTVK--GSWGNDSFALEFGGR 784
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 689 -----MKISAQACYNESITHELTKYRSFKSGFGSGVSHVAVSGEVCASIP 735

Qy 785 LDESALFEQVMPMKLQFYVAHQEGKQGTAREFGSGRLVNLALPIGIRFDKESDC 844
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 736 SNGSGLFSSFSIFSKLQGFSGTQDFEESSEIRSFSSFRNISLPMGITTEKKSQ 795

Qy 845 ATYNLTGLTVDLVRNPDCTTLTIRISGDSWKTFTGNLARQALVLRAGNHFCNS 904
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 796 NYIFYLCAIQDLKRVEGSPVLLKNVSWDAPMANLDSRAMVFLTNQALH-RLQ 854

Qy 905 SQFSFELGSSRNYNVDLGAKYQF 928
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 855 LNVSYVLRGQSHSYSLDLGTYYRF 878
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14

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PM21_CHLPN
ID PM21_CHLPN      STANDARD;      PRT; 1609 AA.
AC Q926U5; Q9RB58;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp21 precursor (Polymorphic membrane
```

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DE protein 21).
GN PM21 OR CPN0963 OR CP0897.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
RN NCBI_TaxID=83558;
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
OLinger L., Grimwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uettermann T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Bisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
(POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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DR EMBL; AB001676; AAD19099.1; -
DR EMBL; AB002248; AAF38684.1; -
DR EMBL; AF002548; BAA99171.1; -
DR FIR; A86611; A86611.
DR FIR; H72013; H72013.
DR PHCI-2DPAGE; Q9RB58; -
DR TIGR; CP0897; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01414; autotrans bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 13.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1609 PROBABLE OUTER MEMBRANE PROTEIN PMP21.
FT CONFLICT 420 420 I -> M (IN REF. 3).
SQ SEQUENCE 1609 AA; 170865 MW; 2604C3E9FC4024CB CRC64;
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Query Match      14.4%; Score 685.5; DB 1; Length 1609;
Best Local Similarity 24.8%; Pred. No. 1.2e-29;
Matches 254; Conservative 144; Mismatches 372; Indels 253; Gaps 36;

Qy 60 VTLENIPGTGTAITSKCF--NNTKGLDFTGTGNLSLLFQTVDAGTVAGAAVNSVVDKST 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 686 VSSDIIRGGGAILAQHIFITDNT--GNLRFSGN-----LGGGESSTV----- 726
```


Job time : 21 secs

Db 2 PLSFKSSPCLLACLSASCAFETRIGGNFVPITNQ--GEEILLTSDFVCNFLG--- 56
Qy 71 AITKSCFNNTKGDILTFTGNNGNSLLFOTVADGTAGAAVNSVVDKSTTFIFGFSLSFIAS 130
Db 57 ASFSSSPINSNSLLGKGLSTFTSCQAPTSNYALLSAA--ETLTFKNFSSINFNGN 114
Qy 131 PGS---SITTKGNVSCSTGSLSTKXVNSLLFSKNPSTDNGGAIATKLTSLTGT---M 183
Db 115 QSTGLGLIYKGOIVFOSIKDLIFTTNRVAYSPASVTTSPAITVTV--TCASALOPT 171
Qy 184 SALFSENST-----SKKGGAIOOTSALTI--TGNQGEVSPSNDTSSDGAAIPTFA 232
Db 172 DSLTVENISQSIKFFGNLANFGSAISSPTAVVKPINNTATMFSFHNFTSSGGGVYGG 231
Qy 233 SVTISNNAK-VSFDINKVTGA-----SSSTTGMMSGGAICAYKTSTDTK----- 275
Db 232 SLLFENNNGCIIIFTANCVNSLKGVTSPSSGYALGSGGAICIPGTGTELNQKCTFSY 291
Qy 276 -----VLTGNQ-MLLFSNNTSTTAGGAIYVKKLELASGGLTLPFRNSVNG 320
Db 292 NGTPNDAGAIYAETCNVGNQGALLDSNTAARNGGAICAKVLNIQGRGPIEFSRN--- 347
Qy 321 GTPKGGAI-----EDSGELSLSADSGDIVFLGNTVWTSTTPCTNRSSIDLGTSAK 372
Db 348 -RAEKGGAIFIGSVGPPAKQTSLTITLASEGNIAFOGN-MLNTKPGI-RNAITVEAGGE 404
Qy 373 MTAIRSAAGRAIYFDPITGSSVTVDVLKVNETPADSALQYNTGNIIFTGEKLSSETAA 432
Db 405 IVSLSAQGGSRLLVFYDPIHSLPTTSPS-----NKDITINANGASGVVFTSKGLSSTELL 460
Qy 433 DSKNLTSLKLOPVTLSGGLTSLKHGVTLOQAFQOADSRLMDVGTTL-----EPAD 485
Db 461 LPANTTITLLGTVKIAGELKITDNVAVNVGLFATQSGGQLTSGGGTGLGATPTGPAA 520
Qy 486 TS-TINNIVINISSIDGAKAKIETKATSKNLTLSGTTILLDPTGT-FYENHSLRNQSY 543
Db 521 VDFITGKLAFPFSFLKDRFVSASVNAGTENVILTALVLDHVDVTDLYDMVSLQSPVAI 580
Qy 544 DILELKASGTVTSTAVTPDPIMGEKFKHYGQGW-----GP----- 579
Db 581 PIAVFKGA-TVTKTGF-PDGEIATPSHYGQKWSYTWSRPLIIPADPGGPPGPPSPSAN 638
Qy 580 ---IVWGTGASTATFNWTKTYIPNPERIGSLVPSLW-----NAFIDISSIHYLMET 630
Db 639 TLAVVNSDILVST-----YILDFERYGEIVSNLSWISFLGNQAFSDI--LQDVILLI 689
Qy 631 ANEGLQGDRAFCAGLSNFFHKDSTKTRGRHLSGGYVIGGNLHTCSDKILSAAFCQLF 690
Db 690 DHFGL-----SITAKALGAYVEHTPRQGEHGFSGRYGQYQAALSNNYTDHTTLGLSFGQLY 745
Qy 691 GRDRDYFAKNQGVYGGTLYYQHNEYIYISLPCKLRPCSLY-----VTEIPVLPSGN 744
Db 746 GKT-----NANPYDSRCSEQMYLLSFTGQFPITVQKSEALISWK 784
Qy 745 LSYTHTDNDLTKY---TTPYTKVSGNDSPALFEGGRAP1---CLDESALFEQY--MP 796
Db 785 AAYGYSKXHLNTYLRPDKAPKQGGQWNNNSYVLSAEHPFLNWCLLTRPLAQAWDLG 844
Qy 797 FMKLQFYVHOGFKQGTREAREFGSSRLVNLALPIGIR-----FDKESDCQDATYNLT 850
Db 845 FISAELGQWQSKFTENGDLQRGFSRGKGVNSLPIGCSQWTPFPKK-----APSTLTIK 900
Qy 851 LGYTVDLVRNPDCTTTLRISGDSWKTFCTNLARQALVLRAGNHFCNSNFEAFSPSPFE 910
Db 901 LAYKPDYRYRNPNNIVTVNSNQESTSISGANLRHGLFVQIHDVVDLTDTOAFLNYTFD 960
Qy 911 LRGSSRNYNVDLGAKYQF 928
Db 961 GKNGFTNHRVSTGLKSTF 978

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OM protein - protein search, using sw model

Run on: December 16, 2003, 10:35:25 ; Search time 45 Seconds

(without alignments)
5321.618 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSPFKEVFSFAIFPLSM.....FELGRSSRYNVDLCAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriaph:*
17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3991	83.6	772	16 Q9RB71	Q9rb71 chlamydia p
2	1915	40.1	926	2 P71135	P71135 chlamydia p
3	1656.5	34.7	839	2 P77792	P77792 chlamydia p
4	1641.5	34.4	847	2 P71132	P71132 chlamydia p
5	1604.5	33.6	846	2 P71133	P71133 chlamydia p
6	1237	25.9	602	2 Q8VU49	Q8vu49 chlamydia p
7	1219.5	25.5	601	2 Q8VLS7	Q8vls7 chlamydia p
8	1175	24.6	700	2 Q8VU50	Q8vu50 chlamydia p
9	1172.5	24.6	581	2 Q8VU48	Q8vu48 chlamydia p
10	1017.5	21.3	445	16 Q9RB67	Q9rb67 chlamydia p
11	935.5	19.6	649	2 P71134	P71134 chlamydia p
12	916	19.2	359	16 Q9J3K6	Q9jsk6 chlamydia p
13	821	17.2	494	16 Q9RB68	Q9rb68 chlamydia p
14	792	16.6	427	16 Q9RB70	Q9rb70 chlamydia p
15	768	16.1	186	16 Q9RB72	Q9rb72 chlamydia p
16	580	12.1	1530	2 Q93Q88	Q93qe8 chlamydia t

17	379.5	7.9	252	2 Q8VLH7	Q8vlh7 chlamydia p
18	372	7.8	257	2 Q8VLF9	Q8vlf9 chlamydia p
19	328	6.9	151	16 Q9JSK7	Q9jsk7 chlamydia p
20	310.5	6.5	1213	16 Q9JH8	Q9jh8 rhizobium l
21	308.5	6.5	162	16 Q9RB69	Q9rb69 chlamydia p
22	307.5	6.4	1713	3 Q8TGE1	Q8tge1 saccharomyc
23	302.5	6.3	3242	2 Q8G9X9	Q8g9x9 escherichia
24	300.5	6.3	2201	2 Q8GF46	Q8gf46 zymomonas m
25	284	5.9	2283	2 Q8VQ99	Q8vg99 staphylococ
26	282.5	5.9	2232	5 Q8IFX6	Q8ifx6 caenorhabdi
27	282	5.9	1341	16 Q8UAU1	Q8uau1 agrobacteri
28	277.5	5.8	1001	3 Q85164	Q85164 saccharomyc
29	275	5.8	1275	5 Q76602	Q76602 caenorhabdi
30	275	5.8	1557	2 Q9RNI2	Q9rni2 haemophilus
31	275	5.8	2554	16 Q8YDM7	Q8ydm7 brucella me
32	274	5.7	2893	16 Q25063	Q25063 helicobacte
33	273	5.7	392	16 Q9Z881	Q9z881 chlamydia p
34	271	5.7	3225	16 Q8PRM0	Q8prmo xanthomonas
35	270	5.7	3420	16 Q8FUS1	Q8fus1 brucella su
36	267.5	5.6	1672	16 Q8Y366	Q8y366 talstonia s
37	267.5	5.6	3961	16 Q8P942	Q8p942 xanthomonas
38	267	5.6	1008	16 Q98KC9	Q98kc9 rhizobium l
39	265.5	5.6	744	3 Q8TFG9	Q8tf99 schizosacch
40	265	5.6	3930	16 Q98820	Q98e20 rhizobium l
41	262.5	5.5	347	16 Q9RB61	Q9rb61 chlamydia p
42	261	5.5	2275	16 Q8NUJ3	Q8nuj3 staphylococ
43	260	5.4	2271	16 Q99QY4	Q99qy4 staphylococ
44	258.5	5.4	888	5 Q25336	Q25336 leishmania
45	256.5	5.4	1758	16 Q9JMS5	Q9jms5 escherichia

ALIGNMENTS

RESULT 1
Q9RB71 ID Q9RB71 PRELIMINARY; PRT; 772 AA.
AC Q9RB71;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Pmp 3.
CN Pmp_3_2
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia. phila.
OX NCBI_TaxID=83558;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shiba T., Ishii K., Hattori M., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AP002545; BAA98226.1;
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter_1.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
SQ SEQUENCE 772 AA; 82931 MW; 484FC56D635801EB CRC64;

Query Match 83.6%; Score 3991; DB 16; Length 772;
Best Local Similarity 99.9%; Pred. No. 3.9e-179;
Matches 771; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 157 LLFSKNPSTNGGAI TAKTULSLGTWTMSALFSENTSSKGGAIQTSDALTITNGQEVSP 216
Db 1 MLFSKNPSTNGGAI TAKTULSLGTWTMSALFSENTSSKGGAIQTSDALTITNGQEVSP 60


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QY 57 KGNVTLENIPGTGTAITKSCFNWTKGDLTFTGNGNSLLPOTVDAGTVAGAAVNSVVDK 116
Db 61 TGNICAYAGLDSGLSSCFTDTAGNLSFLNGYTLTFCFNIITQSSHPCGAI SVSGTNKT 120
QY 117 TTFIGPSSLFIAPOSSITITGAGVSCSGSLTKNVSLLFKSFSTNDGCAITAKTL 176
Db 121 LDISGSLFSCAYCPGA--TGGAIK-AVENTIIDKNSLVFKHCKSTGEGGAIOCKAS 177
QY 177 SLRGTTMSALFSENTSSKKGAIQTSALITITGNGEVSPSNDTSSDGAIAITEASVTI 236
Db 178 S-----SEALKI 185
QY 237 SNNAKVSFDNKVTGASSSTTGDMGGCAICAYKTSTDTKVTLTGNQMLLFSNNTSTAGG 296
Db 186 EN-----NONLVFAENSSSSSG 203
QY 297 AIYVKLELASGGLTLFNRNVNGTAPKGAIAIEDS-GEISLADSGDIVFLGNTVTS 355
Db 204 AIYADKLTIVSGGFTLFSNNSVS-ASSPKGAIICIKDSGGECSLTADLGDITFDGNKI 262
QY 356 T---TPGTRNSSIDLGTSAKMTALRSAGRAIFYDPIITGSSSTTVTDVLKVNETPADSA 412
Db 263 TNGGSPVTNRNSIDLSSGKFTKLNAGEFGIFYDPIITGGG-----DELNINK---QDT 315
QY 413 LQVTGNIIFTEKLSEREAADSKNLTSLLOPVTLSGGTSLKHGVTLOQAFQOQADR 472
Db 316 VDTGKIVFSGERLSDEEKVAANLAKSDFKQPLKIGSGSLILKDGVTLETKSPTQEGAT 375
QY 473 LEMDVGTLEP-----ADTSTINNLINISSIDCA---KKAKIETKATSKNLTSGTITL 524
Db 376 VVMDLGTTLQTPSSGGETITLTNLDINVASLGGGVAPDPKAVEATESKTVIN-AVNL 434
QY 525 LDPGTFTYHNHSLRNQSDVILELK--AGTIVTSTAV-----TPDPMGEKPHYQGWTW 577
Db 435 VDDNGNAYEPILAAQOPPTAIEVRSGSGSITKPTTNLENLYTPPT-----HYGQGNW 488
QY 578 GPIVWGTGAST---TATFNWTKGYTPNPERIGSLVPSNLWNAFIDISSLHYMETANEG 634
Db 489 -TWTWKQSSAQEKTATLTWEQTYGSPNPERQSLVNTLWGSFDIRAIQNLMDISVNG 547
QY 635 LQDRAFWCAGLSNFFHKDSTKTRFRHLSGGYVIGGNLHSCDKILSAACFOLPGRDR 694
Db 548 ADVHRGFWSGLGNFLHKSQDFKFRFNSAGYALGVYAQTPSEDFVFAAFQOLFQK 607
QY 695 DIFVANKQGTIVYGGTYIYQHNETYIISLPCKLRPCSLSYPT-----EIPVLFSG 743
Db 608 DVLVSKNSSTVYAGSIYQH-----ISYWNVTWNTLLQNTLGAEPVLNA 652
QY 744 NLSYTHDNDLTKY-----TTYPTVKSGWGNDSFALEFGGRAPICLDESALFEQYM 795
Db 653 QLAYCHASNKNTMTDVTAPPKTYSBKGDMGNDGCFGEVFAKAPI-ETASLLFDMYS 711
QY 796 PFMKLOFVYAHQBFKEQGT-EAREFGSSRLVNLALPIGIRFQKESDQCDATVNLTLGYT 854
Db 712 PFVKQLVLAHQDDFKENNSDQRYFESNLTNLSMPIGVKLEFKSHKDTASNLTAY 771
QY 855 VDLVRNPDCITTLRLSGDS--WKTFTGLARQALVLRAGNHFCFNSFEPFQSFELR 912
Db 772 PDIVRSNPDCITALLVSPTSVAVWVTKANLARHAFILQAGNYLALTRNTELFSPQFELR 831
QY 913 GSSRNVNVDLGAQYOF 928
Db 832 GSCRTNIDUGSKIQF 847

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RESULT 5

P71133

ID P71133

AC P71133

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE POMP91B precursor.

```

OS Chlamydomydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83555;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RC MEDLINE=96406378; PubMed=8810511;
RA Longbottom D., Russell M., Jones G.E., Lainsor F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins
RL of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RC MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the
RT highly immunogenic cluster of 90-kilodalton envelope proteins from the
RT Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
RL EMBL; U65943; AAC15923.1;
DR InterPro: IPR003368; Chlamydia_PMP.
DR Pfam: PF02415; DUF145; 3.
DR TIGRPFAM; TIGR01376; POMP_repeat; 3.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 846 AA; 90834 MW; 4CDC31DC03C2964E CRC64;

Query Match 33.6%; Score 1604.5; DB 2; Length 846;
Best Local Similarity 38.7%; Pred. No. 2.4e-67;
Matches 368; Conservative 140; Mismatches 269; Indels 173; Gaps 26;

QY 23 TETVLDSASPDGN-KNGNFSVRESQEDAGTTLFKGNVTLENIPGTGTAITKSCFNWTK 81
Db 26 TNETITSDSYNGNVTSDFEVKEF--TSGAIYTCGNVCI-SYAKDPSLNKSCFSETT 82
QY 82 GDLTFTGNSLLPOTVDAGTVAGAAVNSVVDKSTFTIGFS--SLSFTASPGSSITTCG 139
Db 83 ENLSFIGNYTLTFCFNIITQSSHPCGAI SVSGTNKTLTDSGSLFSCAYCCPG---TTGY 139
QY 140 GAVSCSTGSLTKNVSLLFKSFSTNDGCAITAKTLTSLTGTMTSALFSENTSSKKGAI 199
Db 140 GAIQ-TKGITTLKDNSSLVFHKNCSTAGGAIQCK----- 173
QY 200 QTSDALITGNGEVSPSNDTSSDGAIAITEASVTISNNAKVSFDNKVTGASSTGCD 259
Db 174 -----SSSSTAE 180
QY 260 MSGGAI CAYKTSTDTKVTLTGNQMLLFSNNTSTTAGGAIYVKLELASGGLTLFNRNSVN 319
Db 181 LK-----LENNKLVFSENSKEKGAIYADKLTIVSGGTLFNSNVS 224
QY 320 GGTAPKGAIAIEDS-GEISLADSGDIVFLGNTVST---TPGTRNSSIDLGTSAKMTA 375
Db 225 HNNSPKGAIICIKDSGGECSLTANLGDITFDGNKIITNGGSPVTNRNSIDLSSGKFTK 284
QY 376 LRSAAAGRAIFYDPIITGSSSTTVTDVLKVNETPADSALQYTNLIIFTEKLSEREAADS 434
Db 285 LNAKSGFGIFFDPIANTGGSTEI-----ELNKTESDIT--YTKIVFSGEKLSEBKTVP 338
QY 435 KNLTSLKLPVTLSGGTLSLKHGVTLOQAFQOQADSRLEMDVGTTLT-----PADTSTIN 490
Db 339 ANLKSVPKPLKIGAGSLVLDGVTLEAKKITQTKGSTVVMDLGTLTQTPSSGFTITLT 398
QY 491 NLVINISSI---DGAKKAKIETKATSKNLTSLGTTLLDPTGTFYFNHSLRNQSDVILE 547
Db 399 NLDINIASLGGGGTAPAKLATNTASQAISIA-AVNLVNTDSNTYEDPILSASKSFAI- 456
QY 548 LKASGTVTSTAVTPDPMGEKF---HYGYQGTWGPVWGTGAST---TATFNWTKGYI 600
Db 457 ---TATTSSTVTPPETNLKNYTPPTHYQGNW-TVTWKQSSAQEKTATLTWEQTYG 512

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QY 601 PNERIGSLVPSNLWNAFIDISSLHLYMETANEGLQDRAPFCAGLNFHFKDSTKTRRG 660
Db 513 PNERVUGSLVPTNLWGAFTSTRAIONLMDISVNGADYSRGFWSSLANFLNKSGDTRKR 572
QY 661 FRHLGGYVIGGNLHHTCSDKILSAFQCFGRDRDYFVAKNQGTGYGGTLYYQHNETYIS 720
Db 573 FRHHSAGYALGVYAQTPTSDVCSAFCQFQKDKDYFVSKNSSTIYAGSIYQH----- 626
QY 721 LPCKLRPCSLSYVPT-----EIPVLPFGNLSYTHDNDLTKY-----TY 761
Db 627 -----ISYMWNTNLLQNTLGAEPVLVNAQLTYCHASNMMKTNMTNTYTPKNVTP 677
QY 762 PTVKSGMGNDSFALEFGGRAPICLDESALPEQYPMFKLOFYVAHQSGFKEQGT-EAREF 820
Db 678 SEIKGDNDCGVEFGAKAPI-ETASLLFDMYSFVKLQLVHAHQDDFKENNSDQGRYF 736
QY 821 GSRLVNLALPIGIRFDKSDCQDATYNLTGLYTVDLVRSPNDCPTTLRLISGDS--WKTF 878
Db 737 ESNNLTWLSMPIGVKLEKFSKDKTASYNLTLAYAPDIVRSPNDCPTASLLVSPTSVAVWTK 796
QY 879 GTNLARQALVLRAGNHCFSNFEAFSOFSELEGGSSRNYNVDLAKYQF 928
Db 797 ANNLAHAFILQAGNYLALTRENTLFSQFELGSCRTYNIDLGSKIQF 846

RESULT 6
Q8VU49
ID Q8VU49 PRELIMINARY; PRT; 602 AA.
AC Q8VU49
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydia phila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LLG;
RA Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243418; AAL36962.1; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
FT NON_TER 1
SQ SEQUENCE 602 AA; 65562 MW; CA486CFACEC131E2 CRC64;

Query Match 25.9%; Score 1237; DB 2; Length 602;
Best Local Similarity 42.4%; Pred. No. 2.5e-50;
Matches 261; Conservative 104; Mismatches 205; Indels 46; Gaps 14;

QY 344 GDIVLGNVTSTTPGNT---RSSIDLGTSAKTLRSAGRAIFYDPI-TTGSSTTVT 399
Db 2 GDITFDGNKIITSRSSSTVKNSISLGGGKFTKLNAKEGFGIFFDPIANTGDNTEI 61
QY 400 DVLKVNETPADSALQVNTGNIIFTGKLSSETAADSKNLTSKLLQPVTLSSGGLSLKHGVT 459
Db 62 ELNAKE---GGSTTVTKIVFSGEKLSDKEKVADNLKSYFTQPLKIGAGSLVKDGYT 117
QY 460 LQTAQTAQADSRLENDVGTLEPA---DTSTNNLVINISSIDGA-----KKAKIETKAT 512
Db 118 LEAKKYSQTDGTVVMDLGTTLQTSSTGETITLNDINVASLGGGGVADPAKVEAQAS 177
QY 513 SKNLTSLGTTLLDPTGTFVENHSLRNPSQYDILELKASGTVTSTAVTPD-----PIMG 566
Db 178 GKTVTIN-AVNLDVTDGNAYEYPILATSKPFTAIKAGSSGTTTPTDNLKNYTPPT-- 234
QY 567 EKPHYGQGTGPIVNGTGA---TATFNWTKTGYIPNPERIGSLVPSNLWNAFIDISS 623

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Db 235 ---HYGQGNW-TTWKLGTSABSETALTWEQTDYSNPERQGPLVPNTLMGSEFSDIRA 290
QY 624 LHYLMETANEGLQDRAPFCAGLNFHFKDSTKTRRGRHLSGGYVIGGNLHHTCSDKILS 683
Db 291 IQNLIDISVNGADYRGRFVWSGLNLFHKSNGSTKTRFRHHSAGYALGVYAQTSTEDVPS 350
QY 684 AAFQCFGRDRDYFVAKNQGTGYGGTLYYQHNETYISLPCLRPCSLSYVPTIPLVPSG 743
Db 351 AAFQCFGRDRDYFVAKNQGTGYGGTLYYQHNETYISLPCLRPCSLSYVPTIPLVPSG 743
QY 744 NLSYTHDNDLTKY-----TYPTVKGSGMGNDSFALEFGGRAPICLDESALPEQYPM 795
Db 407 QLYYCHASNMMKTNMTNTYTPKNVTLSEIKGDNDCGVEFGAMAPIETPSSFLFDYS 466
QY 796 PFMKLOFYVAHQSGFKEQGT-EAREFGSSRLVNLALPIGIRFDKSDCQDATYNLTGLYT 854
Db 467 PFLQQLVHAHQDDFKENNSDQGRYFESSNLTWLSMPIGKIFERFAVNDVASYHLTAAYA 526
QY 855 VDLVRSPNDCPTTLRLISGDS--WKTFGTNLARQALVLRAGNHCFSNFEAFSOFSELR 912
Db 527 PDIVRSPNDCPTASLLVSPTSVAVWTKANNLARSFAFLQAGNYLALSHNMELFSQGF 586
QY 913 GSSRNYNVDLAKYQF 928
Db 587 GSSRTYNVDLGSKIQF 602

RESULT 7
Q8VL57
ID Q8VL57 PRELIMINARY; PRT; 601 AA.
AC Q8VL57
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydia phila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=POS, and LLG;
RA Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243417; AAL36961.1; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
FT NON_TER 1
SQ SEQUENCE 601 AA; 65476 MW; D6AA97EC9072C757 CRC64;

Query Match 25.5%; Score 1219.5; DB 2; Length 601;
Best Local Similarity 42.0%; Pred. No. 1.6e-49;
Matches 259; Conservative 106; Mismatches 204; Indels 47; Gaps 15;

QY 344 GDIVLGNVTSTTPGNT---RSSIDLGTSAKTLRSAGRAIFYDPI-TTGSSTTVT 399
Db 2 GDITFDGNKIITSRSSSTVKNSISLGGGKFTKLNAKEGFGIFFDPIANTGDNTEI 61
QY 400 DVLKVNETPADSALQVNTGNIIFTGKLSSETAADSKNLTSKLLQPVTLSSGGLSLKHGVT 459
Db 62 ELNAKE---GGSTTVTKIVFSGEKLSDKEKVADNLKSYFTQPLKIGAGSLVKDGYT 117
QY 460 LQTAQTAQADSRLENDVGTLEPA---DTSTNNLVINISSIDGA-----KKAKIETKAT 512
Db 118 LEAKKYSQTDGTVVMDLGTTLQTSSTGETITLNDINVASLGGGGVADPAKVEAQAS 177
QY 513 SKNLTSLGTTLLDPTGTFVENHSLRNPSQYDILELKASGTVTSTAVTPD-----PIMG 566
Db 178 GKTVTIN-AVNLDVTDGNAYEYPILATSKPFTAIKAGSSGTTTPTDNLKNYTPPT-- 234

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107 567 EKHYGQGTWGPVWGTGAST--TATFNWTKTYIPNPERIGSLVSPNSLWNAFIDISS 623
108      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
109 Db      ---HYGYQGNW-TVTWKLGTSAQBETATLTWEQTDYSPNPERQGPLVPKTLWGSFSDIRA 290
110      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
111 Qy      624 LHYLMETANEGLQGDRAFWCAGLNFPHFKDSTKTRRHLSGGVVGGNLTCSDKILS 683
112      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
113 Db      291 IONLIDISVNGADYRGRFWWSGLGNFLHKSQNTKRRFRHHSAGYALGVYAQTSTEDVFS 350
114      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
115 Qy      684 AAFCOLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLPCKLRPCSLSYVPTPIVLFSG 743
116      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
117 Db      351 AAFCOLFGKDKDYFVSKNSSNIYAGSIYYQHLSYWNAMQNLQ---STICAEAPLVNA 406
118      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
119 Qy      744 NLSYTHDNDLTKYIT-----TYPVKGSGWNSDPALEFGGRAPICLDESALFQOYM 795
120      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
121 Db      407 QLTCHASNNMKNMTNTYVPKNVTLSEIKGWDGNCDFGVFGAMAPI-ENASFLFDYIS 465
122      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
123 Qy      796 PFMKLOFYVAHQEGFKQGT-EAREFGSSRLVNLALPIGIRFDKESQCDQDATYNTLGYT 854
124      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
125 Db      466 PFLQQLVHAHQDDPKENNSQGRYFESSNLTLNMPIGIKFERPAYNDVASYHLTRAAYA 525
126      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
127 Qy      855 VDLVRSPDCPTTLRLISGDS--WKTFTGNLARQALVLRAGNHFCFNSNFEAFSOFSELR 912
128      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
129 Db      526 PDIVRSNPDCTASLLVSPSAVWTKANLARSAPMLQAGNVLALSHNMELFSQFGPEIR 585
130      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
131 Qy      913 GSSRNYNVDLGAQYQF 928
132      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
133 Db      586 GSSRTYNDLGSKIQF 601
134      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
135
136 RESULT 8
137 Q8VU50 PRELIMINARY; PRT; 700 AA.
138 ID Q8VU50;
139 AC Q8VU50;
140 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
141 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
142 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
143 DE Putative polymorphic membrane protein (Fragment).
144 OS Chlamydia psittaci (Chlamydia phila psittaci).
145 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
146 OX NCBI_TaxID=83554;
147 RN [1]
148 RP SEQUENCE FROM N.A.
149 RC STRAIN=POS;
150 RA Laroucau K., Souriau A., Rodolakis A.;
151 RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
152 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
153 DR EMBL; AF243415; AAL36959.1; -
154 DR InterPro; IPR003368; Chlamydia_PMP.
155 DR TrEMBL; F02415; DUF145; 1.
156 DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
157 FT NON TER 700 700
158 SQ SEQUENCE 700 AA; 74200 MW; 2C38E504AF48D1D1 CRC64;
159
160 Query Match 24.6%; Score 1175; DB 2; Length 700;
161 Best Local Similarity 35.5%; Pred. No. 2.4e-47;
162 Matches 284; Conservative 120; Mismatches 227; Indels 170; Gaps 25;
163
164 Qy 23 TETVLDSASPDGN-KNGNFSVRESQEDAGTGYLPKGNVLTENIPGTGTAITKSCFNNTK 81
165 Db 26 TNETLSSSYNGVNTSDDFEVKET--TSGAIYTCGNVCI-SYAGKSPINKSCFSETT 82
166
167 Qy 82 GDLTFTGNGNSLLFQWADAGTVAGAAVNSVVDKSTFTFGFSLSFIAFGSGSIITGKA 141
168 Db 83 ENLSFIGNGYTLCFDNIITTAGNPGAINVSGQKTLNVSGLFSFCAHCPGP--TTGYGA 140
169
170 Qy 142 VSCSTGSLTKNVNLLFSKNFSTDNGAITAKTILSTGTTMSALFSENSSKKGAIQT 201
171 Db 141 IQ-----TKGVS-----
172
173 Qy 202 SDALITGTGQGEVFSFSDNTSDSGAAIFTEASVTISNNAKVFIIDNKVTGASSSTTGDM 261
174      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
175
176 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
177      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
178
179 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
180      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
181
182 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
183      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
184
185 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
186      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
187
188 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
189      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
190
191 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
192      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
193
194 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
195      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
196
197 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
198      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
199
200 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
201      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
202
203 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
204      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
205
206 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
207      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
208
209 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
210      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
211
212 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
213      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
214
215 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
216      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
217
218 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
219      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
220
221 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
222      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
223
224 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
225      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
226
227 Db 344 GDVFLGNVTSTTPGNTN---RSSIDLGTSAKMTALRSAGRAIYFYDPI-TTGSSTT 399
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Qy 255 STTGMS-----GGAICAYKTTDTKVTILTCNQMLLFNSNNTSTTAGGA 297
Db 258 NCSGDLTDTNTSLLLOENSTMQGGALC-----STGT-ISTGSDSINVIGNTSGQKGA 312
Qy 298 IYVKKLELASG-GLTLFSRNSVNGGTAPKGGAIATEDSGELSLSDSGDIVFLGNTVTST 356
Db 313 ISASLXILGGQGGALFSNNVVTHAT-PLGGAIFINTGGSILQLFTQGGDIVFEGNQVTTT 371
Qy 357 TPG--TNRSSIDLGTSAKMTALRSAAAGRAIYFYDPITTTGSGSTTVDVLKNVETPADSALQ 414
Db 372 APNATTXRNVIHLSSTAKWTGLAASQGNAIYFYDPITT-NDTGASDNLIRINEVSANOKL- 429
Qy 415 YTGNIITGKLSSTEADSNLTSKLLQPTVTLGGTSLSKHGVTLOQTQAFQADSELE 474
Db 430 -SGSIVFSGERLTAET- AENLTSRINQPTVTLVEGSLVLKQGVTLITQGSQBSFETLL 487
Qy 475 MDVGTTL 481
Db 488 LDLGTSL 494

RESULT 14
Q9RB70 PRELIMINARY; PRT; 427 AA.
AC Q9RB70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polymorphic outer membrane protein G family.
GN PMP_4.1.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AP002545; BAA98227.1; -
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 6.
SQ SEQUENCE 427 AA; 43419 MW; AB4BBEC1594DD2B1 CRC64;

Query Match 16.6%; Score 792; DB 16; Length 427;
Best Local Similarity 44.0%; Pred. No. 1.1e-29;
Matches 198; Conservative 70; Mismatches 146; Indels 36; Gaps 14;

Qy 1 MKSFPKPFVFTFAIFPLSMI-----ATETVLDSSASFDGN-KNGNFSVRESQEDA-GTTY 54
Db 1 MRSFSLLLISSLAFPLMSVSDAADLTLGRDSYNGDTSTTEFTPKAATSDASGTTY 60
Qy 55 LFGKGVLTENIPGCTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAAGAAVNSVVD 114
Db 61 ILDGDVSIQ-AGKQTSLTSCFSNTAGNLATFLNGFSLHFDNIISSTVAGVWVNTAAS 119
Qy 115 KSTTFIGPSSLSFTASPGSSITTKGAVSCSTGSLTKVNSLLFKNFSFTDNGCAITAK 174
Db 120 GITKFGSFTLRMLAAPR---TTGKAIKITDG-LVFESIGNLDLNLNASSENGCAINTK 175
Qy 175 TLSLTGTMSALFNSNTSSKKGAIQTSDALITGNQGVSFSDNTSSDSGAALFTASV 234
Db 176 TLSLTGSTRFVAFNLGSSSQGGALYASGDSVISENAGILSFGNNSATTSAGASGNL 235
Qy 235 TISNNAKVSFTDNKVTGASSSTTGMSCGACAYK--TSTDTKVTLTQNMLLFNSNNTST 292
Db 236 VISNNQNIFFDGCRAK-----TNGGAIIDCNKAGANPDPIILTLSGNESLHFLNNTAG 286
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Qy 293 TAGAIYVKKLELASG-GLTLFSRNSVNGGTAPKGGAIATEDSGELSLSDSGDIVFLGN 351
Db 287 NSGAIYTKLVLSRGEGVLFNNKAARAT-PKGGAIALDSGEISISDALGNLIFEGN 345
Qy 352 TVTSTT---PGTNRSSIDLGTSAKMTALRSAAAGRAIYFYDPITTTGSGSTTVDVLKNVETP 408
Db 346 T-TSTTGSPASVTRNAIDLASNAKFLNLRATRGKRVIFYDPIT---SSGATDKLSLNKAD 401
Qy 409 ADSALQYTGNIITGKLSSTEADSNLTSKLLQPTVTLGGTSLSKHGVTLOQTQAFQADSKULT 438
Db 402 AGSGNTYEGYIVFSGEKLSEV-----RNLT 426

RESULT 15
Q9RB72 PRELIMINARY; PRT; 186 AA.
AC Q9RB72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polymorphic outer membrane protein G family.
GN PMP_3.1.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AP002545; BAA98225.1; -
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
SQ SEQUENCE 186 AA; 19540 MW; 64557A5346533FA3 CRC64;

Query Match 16.1%; Score 768; DB 16; Length 186;
Best Local Similarity 95.1%; Pred. No. 5.1e-29;
Matches 155; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MKSFPKPFVFTFAIFPLSMIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNV 60
Db 10 MKSFPKPFVFTFAIFPLSMIATETVLDSSASFDGNKNGNFSVRESQEDAGTTYLFKGNV 69
Qy 61 TLENIPGCTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAAGAAVNSVVDKSTTFI 120
Db 70 TLENIPGCTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAAGAAVNSVVDKSTTFI 129
Qy 121 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLLFKNFSVLLFSKNF 163
Db 130 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSVCSAKTF 172

Search completed: December 16, 2003, 10:54:02
Job time : 47 secs
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